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<b>(21) International Application Number:</b> PCT/US99/15838 <b>(22) International Filing Date:</b> 14 July 1999 (14.07.99)		<b>(74) Agents:</b> MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).																						
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09/288,946	9 April 1999 (09.04.99)	US																						
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<b>(54) Title:</b> COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER																								
<b>(57) Abstract</b> <p>Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.</p>																								

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## COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

### TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

### SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present

invention provides polypeptides comprising at least a portion of a prostate tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.



Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited

above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic

kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate tumor polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate tumor polypeptide P502S. In each case, the number of  $\gamma$ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate tumor polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8<sup>+</sup> cell line (3A-1) for a representative prostate tumor antigen (P501S). Figure 6A shows the results of a <sup>51</sup>Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12  
SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16  
SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1  
SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9  
SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4  
SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17  
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17  
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12  
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12  
SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862  
SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862  
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13  
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13  
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19  
SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19  
SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25  
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25  
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24  
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24  
SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58  
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SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63  
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63  
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4  
SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4  
SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14  
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14  
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12  
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16  
SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21  
SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48  
SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55  
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2  
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6  
SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858  
SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860  
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864  
SEQ ID NO: 41 is the determined cDNA sequence for P5  
SEQ ID NO: 42 is the determined cDNA sequence for P8  
SEQ ID NO: 43 is the determined cDNA sequence for P9  
SEQ ID NO: 44 is the determined cDNA sequence for P18  
SEQ ID NO: 45 is the determined cDNA sequence for P20  
SEQ ID NO: 46 is the determined cDNA sequence for P29  
SEQ ID NO: 47 is the determined cDNA sequence for P30  
SEQ ID NO: 48 is the determined cDNA sequence for P34  
SEQ ID NO: 49 is the determined cDNA sequence for P36  
SEQ ID NO: 50 is the determined cDNA sequence for P38  
SEQ ID NO: 51 is the determined cDNA sequence for P39  
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SEQ ID NO: 54 is the determined cDNA sequence for P49  
SEQ ID NO: 55 is the determined cDNA sequence for P50  
SEQ ID NO: 56 is the determined cDNA sequence for P53  
SEQ ID NO: 57 is the determined cDNA sequence for P55  
SEQ ID NO: 58 is the determined cDNA sequence for P60  
SEQ ID NO: 59 is the determined cDNA sequence for P64  
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SEQ ID NO: 66 is the determined cDNA sequence for P68  
SEQ ID NO: 67 is the determined cDNA sequence for P80  
SEQ ID NO: 68 is the determined cDNA sequence for P82  
SEQ ID NO: 69 is the determined cDNA sequence for U1-3064  
SEQ ID NO: 70 is the determined cDNA sequence for U1-3065  
SEQ ID NO: 71 is the determined cDNA sequence for V1-3692  
SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905  
SEQ ID NO: 73 is the determined cDNA sequence for V1-3686  
SEQ ID NO: 74 is the determined cDNA sequence for R1-2330  
SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976  
SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

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SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876  
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SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896  
SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761  
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SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280  
SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)  
SEQ ID NO: 108 is the predicted amino acid sequence for F1-12  
SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17  
SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12  
SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862  
SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

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SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6  
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SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-4744  
SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-4774  
SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-4781  
SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-4785  
SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-4787



SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-4796  
SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-4807  
SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810  
SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811  
SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-4876  
SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-4884  
SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-4896  
SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-4761  
SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-4762  
SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766  
SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770  
SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771  
SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772  
SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309  
SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278  
SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288  
SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283  
SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304  
SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296  
SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280  
SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd  
SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con  
SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev  
SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd  
SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev  
SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd  
SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev  
SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd  
SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev  
SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd  
SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev  
SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd  
SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev  
SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev  
SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd  
SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev  
SEQ ID NO: 223 is the determined cDNA sequence for P509S

SEQ ID NO: 224 is the determined cDNA sequence for P510S  
SEQ ID NO: 225 is the determined cDNA sequence for P703DE5  
SEQ ID NO: 226 is the determined cDNA sequence for 9-A11  
SEQ ID NO: 227 is the determined cDNA sequence for 8-C6  
SEQ ID NO: 228 is the determined cDNA sequence for 8-H7  
SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13  
SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14  
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23  
SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24  
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25  
SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30  
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34  
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35  
SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36  
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38  
SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39  
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40  
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41  
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42  
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45  
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46  
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51  
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56  
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64  
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65  
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67  
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76  
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84  
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85  
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86  
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87  
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88  
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1  
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2  
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2  
SEQ ID NO: 259 is the determined cDNA sequence for JP1B1  
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2

SEQ ID NO: 261 is the determined cDNA sequence for JP1D3  
SEQ ID NO: 262 is the determined cDNA sequence for JP1A4  
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5  
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6  
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6  
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5  
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6  
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8  
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7  
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9  
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10  
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9  
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12  
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12  
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11  
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11  
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12  
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12  
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12  
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2  
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1  
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2  
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3  
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4  
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3  
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4  
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6  
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6  
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5  
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8  
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7  
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7  
SEQ ID NO: 293 is the determined cDNA sequence for P8D8  
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7  
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8  
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8  
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10

SEQ ID NO: 298 is the determined cDNA sequence for JP8C10  
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9  
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10  
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9  
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9  
SEQ ID NO: 303 is the determined cDNA sequence for JP8C12  
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11  
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12  
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12  
SEQ ID NO: 307 is the determined cDNA sequence for P711P  
SEQ ID NO: 308 is the determined cDNA sequence for P712P  
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23  
SEQ ID NO: 310 is the determined cDNA sequence for P774P  
SEQ ID NO: 311 is the determined cDNA sequence for P775P  
SEQ ID NO: 312 is the determined cDNA sequence for P715P  
SEQ ID NO: 313 is the determined cDNA sequence for P710P  
SEQ ID NO: 314 is the determined cDNA sequence for P767P  
SEQ ID NO: 315 is the determined cDNA sequence for P768P  
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes  
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5  
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5  
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26  
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26  
SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23  
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23  
SEQ ID NO: 332 is the determined full length cDNA sequence for P509S  
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)  
SEQ ID NO: 334 is the determined cDNA sequence for P714P  
SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)  
SEQ ID NO: 336 is the predicted amino acid sequence for P705P  
SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10  
SEQ ID NO: 338 is the amino acid sequence of the peptide p5  
SEQ ID NO: 339 is the predicted amino acid sequence of P509S  
SEQ ID NO: 340 is the determined cDNA sequence for P778P  
SEQ ID NO: 341 is the determined cDNA sequence for P786P  
SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteasome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO:386 is the cDNA sequence for 23320.

SEQ ID NO:387 is the cDNA sequence for CGI-69.

SEQ ID NO:388 is the cDNA sequence for L-idoitol-2-dehydrogenase.

SEQ ID NO:389 is the cDNA sequence for 23379.

SEQ ID NO:390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553.

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.  
SEQ ID NO:415 is the cDNA sequence for 22572.  
SEQ ID NO:416 is the cDNA sequence for 22573.  
SEQ ID NO:417 is the cDNA sequence for 22573.  
SEQ ID NO:418 is the cDNA sequence for 22575.  
SEQ ID NO:419 is the cDNA sequence for 22580.  
SEQ ID NO:420 is the cDNA sequence for 22581.  
SEQ ID NO:421 is the cDNA sequence for 22582.  
SEQ ID NO:422 is the cDNA sequence for 22583.  
SEQ ID NO:423 is the cDNA sequence for 22584.  
SEQ ID NO:424 is the cDNA sequence for 22585.  
SEQ ID NO:425 is the cDNA sequence for 22586.  
SEQ ID NO:426 is the cDNA sequence for 22587.  
SEQ ID NO:427 is the cDNA sequence for 22588.  
SEQ ID NO:428 is the cDNA sequence for 22589.  
SEQ ID NO:429 is the cDNA sequence for 22590.  
SEQ ID NO:430 is the cDNA sequence for 22591.  
SEQ ID NO:431 is the cDNA sequence for 22592.  
SEQ ID NO:432 is the cDNA sequence for 22593.  
SEQ ID NO:433 is the cDNA sequence for 22594.  
SEQ ID NO:434 is the cDNA sequence for 22595.  
SEQ ID NO:435 is the cDNA sequence for 22596.  
SEQ ID NO:436 is the cDNA sequence for 22847.  
SEQ ID NO:437 is the cDNA sequence for 22848.  
SEQ ID NO:438 is the cDNA sequence for 22849.  
SEQ ID NO:439 is the cDNA sequence for 22851.  
SEQ ID NO:440 is the cDNA sequence for 22852.  
SEQ ID NO:441 is the cDNA sequence for 22853.  
SEQ ID NO:442 is the cDNA sequence for 22854.  
SEQ ID NO:443 is the cDNA sequence for 22855.  
SEQ ID NO:444 is the cDNA sequence for 22856.  
SEQ ID NO:445 is the cDNA sequence for 22857.  
SEQ ID NO:446 is the cDNA sequence for 23601.  
SEQ ID NO:447 is the cDNA sequence for 23602.  
SEQ ID NO:448 is the cDNA sequence for 23605.  
SEQ ID NO:449 is the cDNA sequence for 23606.  
SEQ ID NO:450 is the cDNA sequence for 23612.

SEQ ID NO:451 is the cDNA sequence for 23614.  
SEQ ID NO:452 is the cDNA sequence for 23618.  
SEQ ID NO:453 is the cDNA sequence for 23622.  
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.  
SEQ ID NO:455 is the cDNA sequence for LIM protein.  
SEQ ID NO:456 is the cDNA sequence for a known gene.  
SEQ ID NO:457 is the cDNA sequence for a known gene.  
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.  
SEQ ID NO:459 is the cDNA sequence for 23045.  
SEQ ID NO:460 is the cDNA sequence for 23032.  
SEQ ID NO:461 is the cDNA sequence for 23054.  
SEQ ID NOs:462-467 are cDNA sequences for known genes.  
SEQ ID NOs:468-471 are cDNA sequences for P710P.  
SEQ ID NO:472 is a cDNA sequence for P1001C.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate tumor protein or a variant thereof. A "prostate tumor protein" is a protein that is expressed in prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain prostate tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.



The present invention is based on the discovery of human prostate tumor proteins. Sequences of polynucleotides encoding certain tumor proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Sequences of polypeptides comprising at least a portion of a tumor protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

#### PROSTATE TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50,

in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenesis pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to

the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using

standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate tumor protein are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Isolation of these

polynucleotides is described below. Each of these prostate tumor proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such

as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (*e.g.*, avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

#### PROSTATE TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate tumor protein or a variant thereof, as described herein. As noted above, a "prostate tumor protein" is a protein that is expressed by prostate tumor cells. Proteins that are prostate tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from

the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein.

Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are



*E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into

the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as

amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

#### BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, urine and/or tumor biopsies) from

patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g., mice, rats, rabbits, sheep or goats*). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e., reactivity with the polypeptide of interest*). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient

time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and

thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

#### T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (*see also* U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate tumor polypeptide, polynucleotide encoding a prostate tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience

(Greene 1998)). T cells that have been activated in response to a prostate tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Prostate tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a prostate tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

#### PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998,



and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or

preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- $\beta$ ) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is

quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-

surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS,  $\alpha$ 13 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a prostate tumor protein (or portion or other variant thereof) such that the prostate tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that

provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

#### CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein

may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100  $\mu$ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such

a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

#### METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g., Harlow and Lanc, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding

agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.



More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred

embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate tumor polypeptides to

detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a prostate tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate tumor polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate tumor polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers

comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375 and 381. Techniques for both PCR based assays and hybridization assays are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, 1987; Erlich ed., PCR Technology, Stockton Press, NY, 1989*).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

## DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

## EXAMPLES

### EXAMPLE 1

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of

H<sub>2</sub>O, heat-denatured and mixed with 100  $\mu$ l (100  $\mu$ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50  $\mu$ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23  $\mu$ l H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10  $\mu$ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5  $\mu$ l H<sub>2</sub>O. Tracer DNA was mixed with 15  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12  $\mu$ l H<sub>2</sub>O, mixed with 8  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human

autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted



amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO: 73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and

prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339.

## EXAMPLE 2

### DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that

F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression

in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney). The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

### EXAMPLE 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated

and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable.

Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX\_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues.



Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

#### EXAMPLE 4

#### SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

#### EXAMPLE 5

##### FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350-365.

#### EXAMPLE 6

##### PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2.1 (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A<sup>b</sup> binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL),  $2 \times 10^{-5}$  M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml  $\beta$ 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells ( $5 \times 10^5$ /ml) were restimulated with  $2.5 \times 10^6$ /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were

restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2.1 expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2.1 molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 µg/ml were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2.1 were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5µg of P1S #10 and 120µg of an I-A<sup>b</sup> binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2µg/ml P1S#10 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later cells ( $5 \times 10^5$ /ml) were restimulated with  $2.5 \times 10^6$ /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly

basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

#### EXAMPLE 7

##### ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE TUMOR POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8<sup>+</sup> T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8<sup>+</sup> T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a  $\gamma$ -interferon ELISPOT assay (see Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on  $10^4$  fibroblasts in the presence of 3  $\mu$ g/ml human  $\beta_2$ -microglobulin and 1  $\mu$ g/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml  $\gamma$ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a  $\gamma$ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of  $\gamma$ -interferon spots with increasing numbers of T

cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

#### EXAMPLE 8

##### PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate tumor antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg VR10132-P501S either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed A2-restricted CTL epitope.

#### EXAMPLE 9

##### GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH PROSTATE TUMOR ANTIGEN

Using *in vitro* whole-gene priming with P501S-retrovirally transduced autologous fibroblasts (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above. Using a panel of HLA-mismatched fibroblast lines transduced with P501S, these CTL lines were shown to be restricted HLA-A2 class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 µg/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8<sup>+</sup> T cells were isolated using a magnetic bead system, and

priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S. Following four stimulation cycles, CD8+ T cell lines were identified that specifically produced interferon- $\gamma$  when stimulated with P501S-transduced autologous fibroblasts. The P501S-specific activity could be sustained by the continued stimulation of the cultures with P501S-transduced fibroblasts in the presence of IL-15. A panel of HLA-mismatched fibroblast lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- $\gamma$  in an ELISPOT assay, the P501S specific response was shown to be restricted by HLA-A2. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

#### EXAMPLE 10

##### IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE TUMOR ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2 transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of P703P transduced target cells expressing either HLA-A2Kb or HLA-A2. Specifically, HLA-A2 transgenic mice were immunized subcutaneously in the footpad with 100  $\mu$ g of p5 peptide together with 140  $\mu$ g of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with p5 peptide and cultured with GM-CSF and IL-4 together with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis



with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated.

#### EXAMPLE 11

##### EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate tumor and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

#### EXAMPLE 12

##### ELICITATION OF PROSTATE TUMOR ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate tumor antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GM-CSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8<sup>+</sup> cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles, CD8<sup>+</sup> lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to

express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays ( $^{51}\text{Cr}$  release) and interferon-gamma production (Interferon-gamma Elispot; *see above* and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

### EXAMPLE 13

#### IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

Table I  
Summary of Prostate Tumor Antigens

Known Genes	Previously identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang(23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	

transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-Iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate

tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

#### EXAMPLE 14

##### IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate tumor antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups, Plus (normal prostate and prostate tumor libraries, and breast cell lines, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

**Table II**  
Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones found in the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones found in the Plus, Minus and Other group libraries, but the expression in the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones found in Plus, Minus and Other group libraries, but the expression in the Plus group is higher than the expression in the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III  
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor cDNA was at least three times the level in normal prostate cDNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NOs:401-453, with certain novel sequences shown in SEQ ID NOs:407, 413, 416-419, 422, 426, 427 and 450.

Table IV  
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P

403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57



439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

#### EXAMPLE 15

##### FURTHER IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NOs:454-467. Of these sequences SEQ ID NOs:459-461 correspond to novel genes. The others (SEQ ID NOs:454-458 and 461-467) correspond to known sequences.

#### EXAMPLE 16

##### FURTHER CHARACTERIZATION OF PROSTATE TUMOR ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic ABI Sequencer. Four sequences were obtained, and are presented in SEQ ID NOs:468-471.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

## CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339 and 383.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a prostate tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434,

435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

7. An isolated polynucleotide comprising a sequence that hybridizes, under moderately stringent conditions, to a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-7.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An expression vector comprising a polynucleotide according claim 8.

12. A host cell transformed or transfected with an expression vector according to claim 11.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, in combination with a physiologically acceptable carrier.

14. A vaccine comprising a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

15. A vaccine according to claim 14, wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine according to claim 14, wherein the non-specific immune response enhancer induces a predominantly Type I response.

17. A pharmaceutical composition comprising a polynucleotide according to claim 4, in combination with a physiologically acceptable carrier.

18. A vaccine comprising a polynucleotide according to claim 4, in combination with a non-specific immune response enhancer.

19. A vaccine according to claim 18, wherein the non-specific immune response enhancer is an adjuvant.

20. A vaccine according to claim 18, wherein the non-specific immune response enhancer induces a predominantly Type I response.

21. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472 or a complement of any of the foregoing polynucleotide sequences.

22. A pharmaceutical composition comprising an antibody or fragment thereof according to claim 18, in combination with a physiologically acceptable carrier.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

26. A vaccine according to claim 25, wherein the non-specific immune response enhancer is an adjuvant.

27. A vaccine according to claim 25, wherein the non-specific immune response enhancer induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

30. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polynucleotide according to claim 4, and thereby inhibiting the development of a cancer in the patient.

31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antibody or antigen-binding fragment thereof according to claim 21, and thereby inhibiting the development of a cancer in the patient.

32. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

33. A method according to claim 32, wherein the antigen-presenting cell is a dendritic cell.

34. A method according to any one of claims 29-32, wherein the cancer is prostate cancer.

35. A fusion protein comprising at least one polypeptide according to claim 1.

36. A fusion protein according to claim 35, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

37. A fusion protein according to claim 35, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

38. A fusion protein according to claim 35, wherein the fusion protein comprises an affinity tag.

39. An isolated polynucleotide encoding a fusion protein according to claim 35.

40. A pharmaceutical composition comprising a fusion protein according to claim 32, in combination with a physiologically acceptable carrier.

41. A vaccine comprising a fusion protein according to claim 35, in combination with a non-specific immune response enhancer.

42. A vaccine according to claim 41, wherein the non-specific immune response enhancer is an adjuvant.

43. A vaccine according to claim 41, wherein the non-specific immune response enhancer induces a predominantly Type I response.

44. A pharmaceutical composition comprising a polynucleotide according to claim 40, in combination with a physiologically acceptable carrier.

45. A vaccine comprising a polynucleotide according to claim 40, in combination with a non-specific immune response enhancer.

46. A vaccine according to claim 45, wherein the non-specific immune response enhancer is an adjuvant.

47. A vaccine according to claim 45, wherein the non-specific immune response enhancer induces a predominantly Type I response.

48. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 40 or claim 44.

49. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 41 or claim 45.

50. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;  
wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate tumor protein from the sample.

51. A method according to claim 50, wherein the biological sample is blood or a fraction thereof.



52. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

53. A method for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of:

- (i) a polypeptide according to claim 1;
  - (ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
  - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); and/or
  - (iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii);
- under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

54. An isolated T cell population, comprising T cells prepared according to the method of claim 53.

55. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 54.

56. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

57. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

- (b) cloning at least one proliferated cell; and
- (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

58. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

- (ii) complements of the foregoing polynucleotides;
- (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

59. A method according to claim 58, wherein the binding agent is an antibody.

60. A method according to claim 59, wherein the antibody is a monoclonal antibody.

61. A method according to claim 58, wherein the cancer is prostate cancer.
62. A method for monitoring the progression of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
  - (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
  - (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
  - (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.
63. A method according to claim 62, wherein the binding agent is an antibody.
64. A method according to claim 63, wherein the antibody is a monoclonal antibody.
65. A method according to claim 62, wherein the cancer is a prostate cancer.
66. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
  - (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

67. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

68. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

69. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

70. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

71. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

72. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 21; and
- (b) a detection reagent comprising a reporter group.

73. A kit according to claim 72, wherein the antibodies are immobilized on a solid support.

74. A kit according to claim 73, wherein the solid support comprises nitrocellulose, latex or a plastic material.

75. A kit according to claim 72, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

76. A kit according to claim 72, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

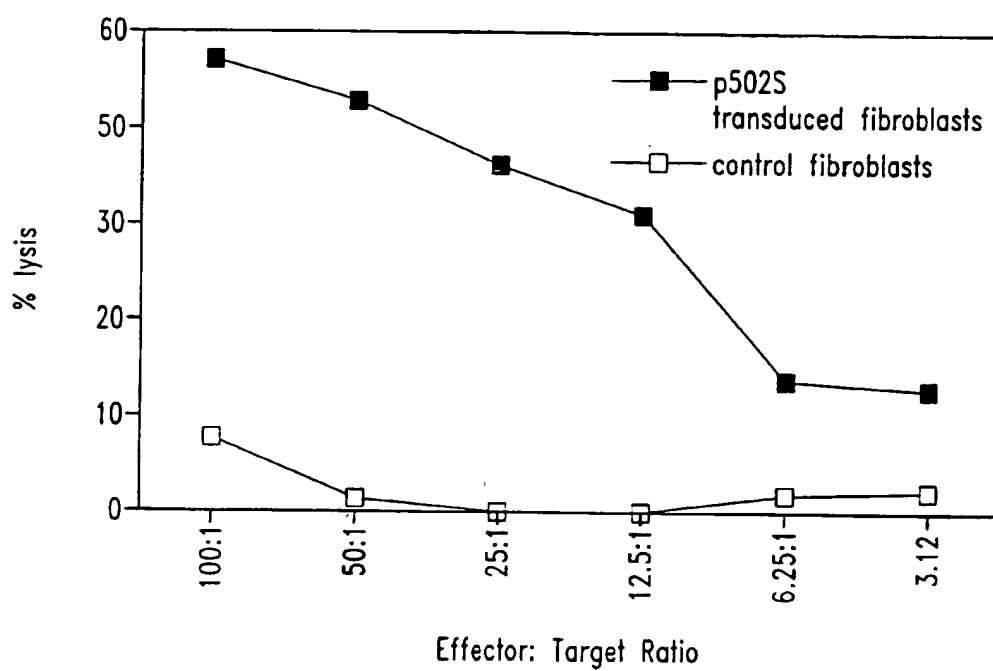
77. An oligonucleotide comprising 10 to 40 nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotides.

78. A oligonucleotide according to claim 77, wherein the oligonucleotide comprises 10-40 nucleotides recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

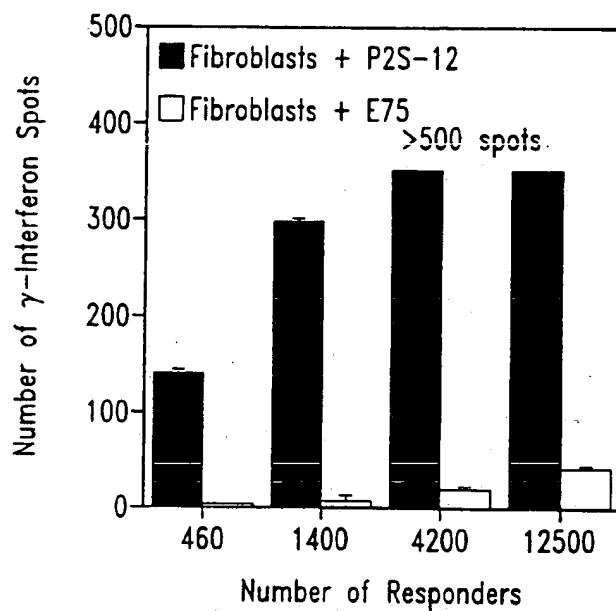
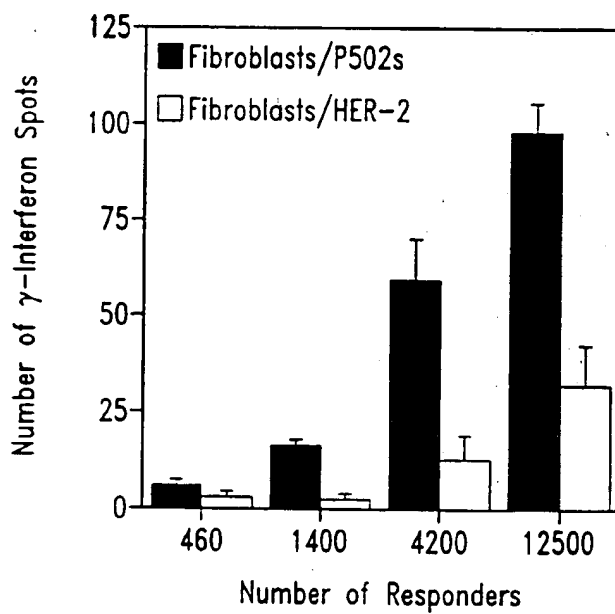
79. A diagnostic kit, comprising:

- (a) an oligonucleotide according to claim 77; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

1/5

*Fig. 1*

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*Fig. 2A**Fig. 2B*

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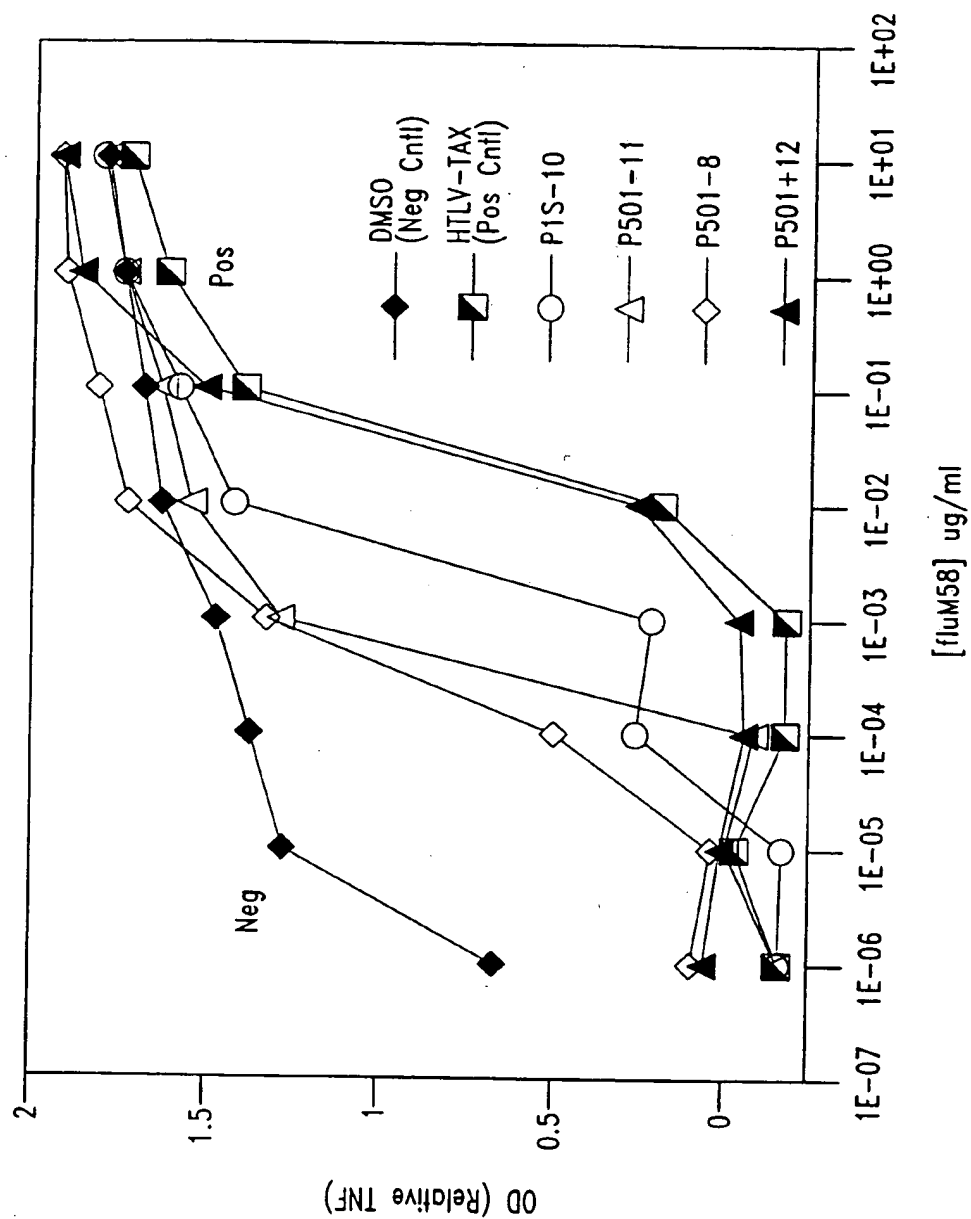
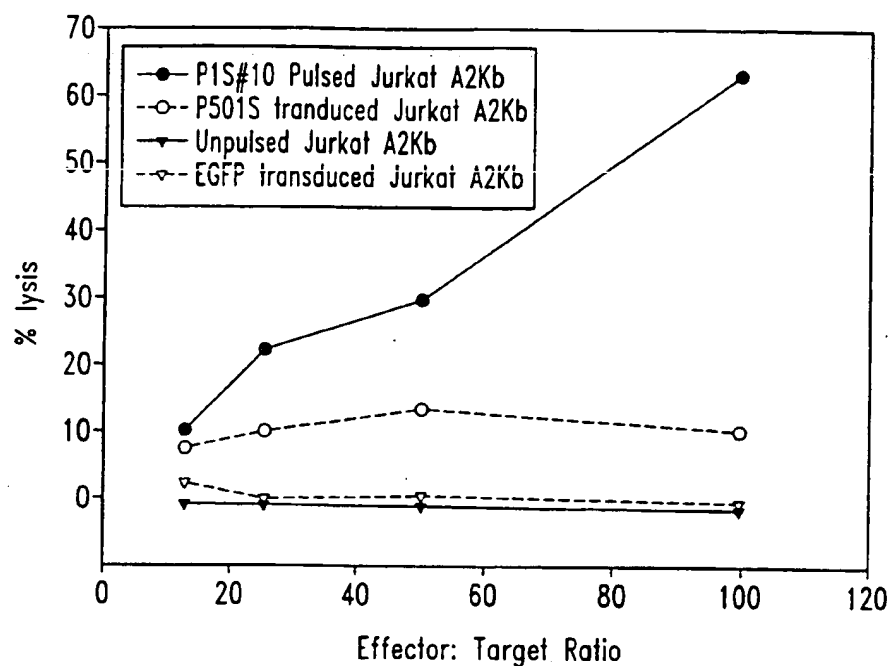
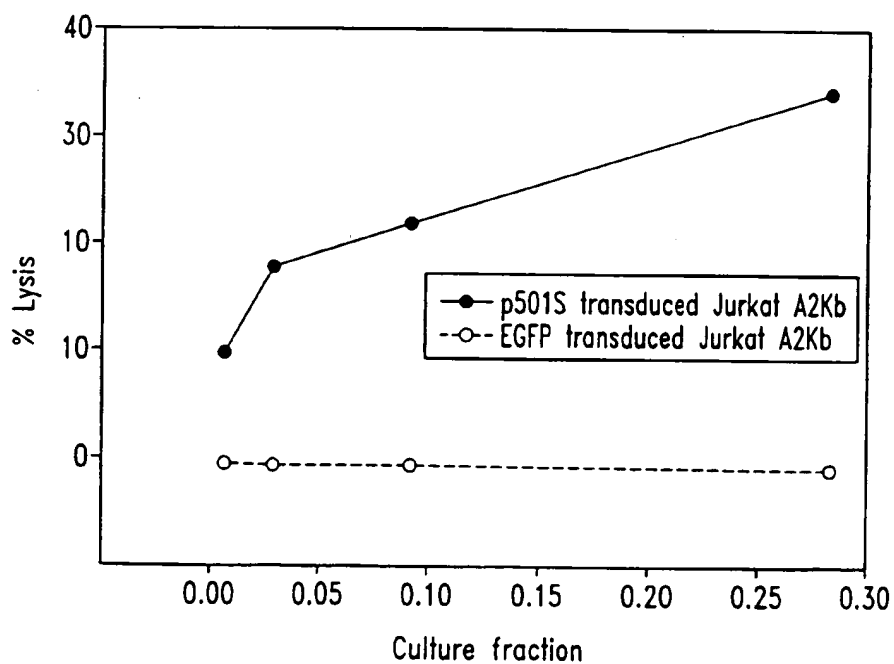


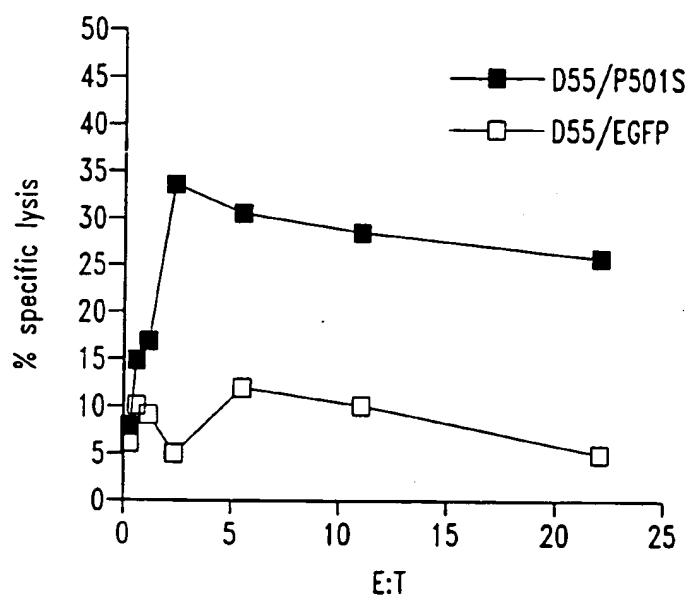
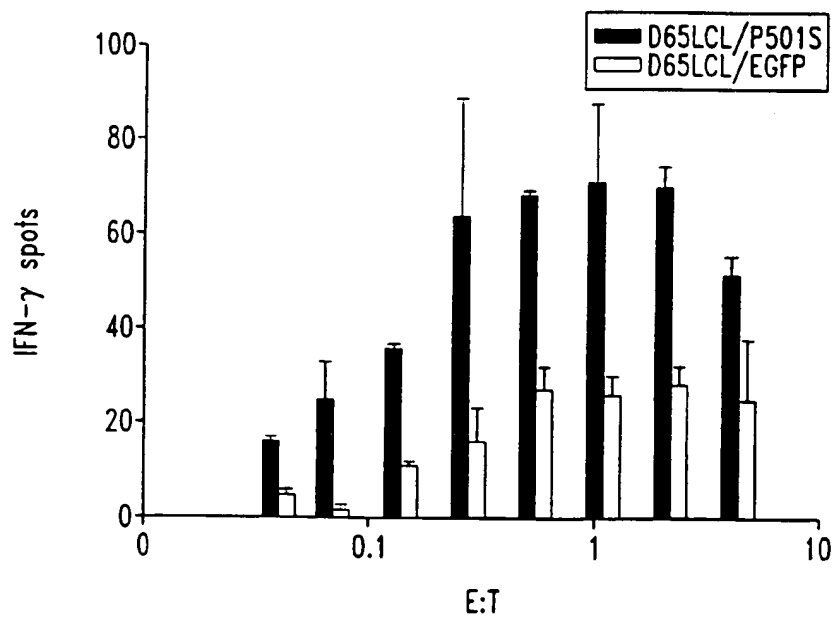
Fig. 3



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*Fig. 4**Fig. 5*

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*Fig. 6**Fig. 7*

## SEQUENCE LISTING

&lt;110&gt; Corixa Corporation

<120> COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
OF PROSTATE CANCER AND METHODS FOR THEIR USE

&lt;130&gt; 210121.42701PC

&lt;140&gt; PCT

&lt;141&gt; 1999-07-08

&lt;160&gt; 472

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 814

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(814)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1

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ccaggggggc	cagtccctct	ccttacttca	tccccatccc	atgccaaagg	aagaccctcc	180
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tcttccgctt	ctcgctcact	nantcctgcg	ctcggtcctt	cggctgcggg	gaacggtatc	720
actcctcaaa	ggnggtatta	cggttatccn	naaatcnggg	gatacccnng	aaaaaanttt	780
aacaaaaggg	cancaaaggg	cngaaacgta	aaaa			814

&lt;210&gt; 2

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(816)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 2

acagaaatgt	tggatggtgg	agcacctttc	tatacgactt	acaggacagc	agatggggaa	60
ttcatggctg	ttggagcaat	agaacccccag	ttctacgagc	tgctgatcaa	aggactrgga	120

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ctaaagtctg atgaacttcc caatcagatg agcatggatg attggccaga aatgaagaag      180
aagtttgcag atgtatttgc aaagaagacg aaggcagagt ggtgtcaa atttgacggc      240
acagatgcct gtgtgactcc ggttctgact tttagaggagg ttgttcatca tgatcacaac      300
aaggaacggg gctcgtttat caccagttag gagcaggacg tgagcccccg ccctgcacct      360
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gccgccaccg cgggtggagct ccagctttttg ttcccttttag tgagggttaa ttgcgcgctt      480
ggcgtaatca tggtcatagc tgtttcctgt gtgaaattgt tatccgctca caattccccc      540
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cattaattgc gttgcgctca ctgcccgtt tccagtcggg aaaactgtcg tgccactgen      660
ttantgaatc ngccaccccc cgggaaaagg cgggttgcntt ttgggctct tccgctttcc      720
tcgctcattg atcctngcnc ccggtcttcg gctgcggnga acggttcact cctcaaaggc      780
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&lt;210&gt; 3

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(773)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 3

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cttttgaaag aagggatggc tggggtgttt aacagcagag gtgcagggcg ggggctcacg      60
tctgtctcct cactgggtgat aaacgagccc cgttccttgt tgtgatcatg atgaacaacc      120
tcttcaaaag tcagaaccgg agtcacacag gcatctgtgc cgtcaaagat ttgacaccac      180
tctgccttcg tcttctttgc aaatacatct gcaaacttct tcttcatttc tggccaatca      240
tccatgctca tctgattggg aagttcatca gacttttagtc canntccttt gatcagcagc      300
tcgtagaact ggggttctat tgcctcaaca gccatgaatt ccccatctgc tgtcctgtaa      360
gtcgtataga aagggtgctcc accatccaac atgttctgtc ctgcaggggg ggcccggtaac      420
ccaattcgcc ctatantgag tcgtattacg cgcgctcact ggccgtcgtt ttacaacgtc      480
gtgactggga aaaccctggg cgttaccaac ttaatcgctt tgcagcacat ccccttttcg      540
ccagctgggc gtaatanaga aaaggccgc accgatcgcc cttccaacag ttgcgcacct      600
gaatgggnaa atgggacccc cctgttacg cgcattnaac ccccgcnngg tttngttggt      660
acccccacnt nnaccgctta cactttgcca gcgccttanc gcccgctccc tttcnccttt      720
cttcccttcc tttcncncn ctttcccccg ggggttcccc cntcaaacc cna                                773

```

&lt;210&gt; 4

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(828)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 4

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cctcctgagt cctactgacc tgtgctttct ggtgtggagt ccagggtgc taggaaaagg      60
aatgggcaga cacaggtgta tgccaatgtt tctgaaatgg gtataatttc gtctctcct      120
tcggaacact ggctgtctct gaagacttct cgctcagttt cagtgaggac acacacaaag      180
acgtgggtga ccatgttggt tgtgggtgac agagatggga ggggtggggc ccaccctgga      240
agagtggaca gtgacacaag gtggacactc tctacagatc actgaggata agctggagcc      300
acaatgcatt aggcacacac acagcaagga tgacnctgta aacatagccc acgtgtcct      360

```

```

gnngggcactg ggaagcctan atnaggccgt gagcanaaag aaggggagga tccactagtt      420
ctanagcggc cgccaccgcg gtgganctcc ancttttggt cccttttagtg agggttaatt      480
gcgcgcttgg cntaatcatg gtcatanctn tttcctgtgt gaaattgtta tccgctcaca      540
attccacaca acatacgaac cggaaacata aantgtaaac ctggggtgcc taatgantga      600
ctaactcaca ttaattgcgt tgcgctcact gcccgtttc caatcnggaa acctgtcttg      660
ccncttgcat tnatgaatcn gccaaccccc ggggaaaagc gtttgcggtt tgggcgctct      720
tccgcttctt cncctantta ntccctncnc tcggtcattc cggctgcngc aaaccgggtt      780
accnctcca aaggggggtat tccggtttcc ccnaatccgg gganancc                    828

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<210> 5

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

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<223> n = A,T,C or G

<400> 5

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attttataac aatcaacacc tgtggctttt aaaatttggg tttcataaga taattttatac      180
tgaagtaaatt ctagccatgc ttttaaaaaa tgcttttaggt cactccaagc ttggcagtta      240
acatttgcca taaacaataa taaaacaatc acaatttaat aaataacaaa tacaacattg      300
taggccataa tcatatacag tataaggaaa aggtggtagt gttgagtaag cagttattag      360
aatagaatac cttggcctct atgcaaatat gtctagacac tttgattcac tcagccctga      420
cattcagttt tcaaagtagg agacagggtc tacagtatca ttttacagtt tccaacacat      480
tgaaaacaag tagaaaatga tgagttgatt tttattaatg cattacatcc tcaagagtta      540
tcaccaaccc ctgagttata aaaaattttc aagttatatt agtcataaa cttggtgtgc      600
ttatttttaa ttagtgctaa atggattaag tgaagacaac aatgggtccc taatgtgatt      660
gatattggtc atttttacca gcttctaaat ctnaactttc aggccttttg actggaacat      720
tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa      780
tgttattttg ttaaaaatta aattttaacc tgggtgaaaa ataatttgaa atna                    834

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<210> 6

<211> 818

<212> DNA (

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(818)

<223> n = A,T,C or G

<400> 6

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aaccacatct acaaaatgcc agtatcaggc ggcggcttcg aagccaaagt gatgtttgga      120
tgtaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagttg agccaataat      180
gacgtgaagt ccgtggaagc ctgtggctac aaaaaatgtt gagccgtaga tgccgtcggg      240
aatggtgaag ggagactcga agtactctga ggcttgtagg agggtaaaat agagaccag      300
taaaattgta ataagcagtg cttgaattat ttggtttcgg ttggttttcta ttagactatg      360
gtgagctcag gtgattgata ctctgatgc gagtaatacg gatgtgttta ggagtgggac      420
ttctagggga tttagcgggg tgatgcctgt tgggggccag tgccctccta gttggggggg      480
aggggctagg ctggagtggc aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga      540

```

```

ggtaataaat aggattatcc cgtatcgaag gccttttttg acaggtggtg tgtggtggcc      600
ttggtatgtg ctttctcgtg ttacatcgcg ccatcattgg tatatgggta gtgtgttggg      660
ttantanggc ctantatgaa gaacttttgg antggaatta aatcaatngc ttggccggaa      720
gtcattanga nggctnaaaa ggccctgtta nggggtctggg ctnggtttta cccnaccat      780
ggaatncncc ccccggaacna ntgnatccct attcttaa                               818

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&lt;210&gt; 7

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(817)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 7

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cgggcccctat ttcaaagatt tttaggggaa ttaattctag gacgatgggt atgaaactgt     120
ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcgggta      180
aagtggtttg gtttagacgt ccgggaattg catctgtttt taagcctaata gtggggacag      240
ctcatgagtg caagacgtct tgtgatgtaa ttattatacn aatgggggct tcaatcggga      300
gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tggttctagg aataatgggg      360
gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc      420
attgggtggc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa      480
aggatncctt ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangatatt      540
tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaaan tttngttatt      600
gaatnttnng gaaaagggct tacaggacta gaaaccaaata angaaaanta atnntaangg      660
cnttatcntn aaaggtmata accnctccta tnatcccacc caatngnatt cccacncnn      720
acnattggat ncccanttc canaaanggc cccccccgg tgnannccnc cttttgttcc      780
cttnantgan ggttattcnc cctngcmtt atcanc                               817

```

&lt;210&gt; 8

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(799)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 8

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catttcgggg tttactttct aaggaaagcc gagcgggaagc tgctaactgt ggaatcgggt      60
cataaggaga actttctgct ggcacgcgct agggacaagc gggagagcga ctccgagcgt     120
ctgaagcgca cgtcccagaa ggtggacttg gcactgaaac agctgggaca catccgcgag      180
tacgaacagc gcctgaaagt gctggagcgg gaggtccagc agttagccg cgtcctgggg      240
tggttgcccg angcctganc cgctctgcct tgctgcccc angtgggccg ccacccctg      300
acctgcctgg gtccaaacac tgagccctgc tggcggactt caagganaac cccacangg      360
ggattttgct cctanantaa ggctcatctg ggctcgggccc ccccccactg gttggccttg      420
tctttgangt gagcccatg tccatctggg cactgtcng gaccaccttt ngggagtgtt      480
ctccttaciaa ccacannaag cccggctcct cccggaaacc antccancc tngnaaggat      540
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tccttttctn tnagggttaa tnnccgcttg gccctnccan ngtcctncc ntttccnnt      660
gttnaaattg ttangcnccc nccnntcccn cncnncnan cccgaccenn annttnnann      720

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nccctgggggt nccnnngat tgaccenncc nccctntant tgcnttnggg nncnntgccc 780  
ctttccctct nggganncg 799

<210> 9

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(801)

<223> n = A,T,C or G

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taangatgac actcccaaag gtggtcctga cagtggccca gatggacatg gggctcacct	120
caaggacaag gccaccaggt gcgggggccc aagcccacat gatccttact ctatgagcaa	180
aatcccctgt gggggcttct ccttgaagtc cgccancagg gctcagtctt tggacccang	240
caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcncg gggcctcngn	300
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ttcntaccgg cgnatntgtc ccantgttt cngtgccnac tccancttct nggacgtgcg	420
ctacatacgc ccggantcnc nctcccgtt tgtccctatc cacgtncan caacaaattt	480
cncntantg caccnattcc cacntttnc agnttccnc nncgngcttc cttntaaaag	540
ggttgancec cggaatatnc cccaaagggg gggggccngg taccaaactn cccctnata	600
gctgaantcc ccatnaccnn gnctcnatgg anccntcent ttaannacn tctnaactt	660
gggaanance ctcgncentn ccccnttaa tccnccttg cnangnnent ccccnntcc	720
nccnnntng gcntntnann cnaaaaaggc ccnnnancan tctcctnnn cctcanttcg	780
ccanccctcg aaatcgccn c	801

<210> 10

<211> 789

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(789)

<223> n = A,T,C or G

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agatcctgcc ctacacactg gcctccctct accaccggga gaagcaggtg ttctgccc	180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttctgc	240
caggccctaa gcctggagct ccctcccta atggacacgt ggggtgctgga ggcagtggcc	300
tgtcccccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg	360
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ccatcctgga tagtgcttcc tgtgtccca ngtggcccca tccctgttta tgggtctccat	480
tgtccagctc agccagtctg tcaactgccta tatggtgtct gccgcaggcc tgggtctggt	540
cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg	600
ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactccccgc	660
tcctgttaac cccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaanat	720
gtggtctctc gctgccacct gttgctggct gaagtgcnta cngcncant nggggggtrg	780
gnggttccc	789

<210> 11  
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 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(772)  
 <223> n = A,T,C or G

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 accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180  
 tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata 240  
 actttcatat gttcaaatacc catggaggag tgtttcatcc tagaaactcc catgcaagag 300  
 ctacattaaa cgaagctgca ggtaagggg cttanagatg ggaaaccagg tgactgagtt 360  
 tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420  
 ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480  
 ctccctgtat aagtccagac tgaaccccc ttggaaggnc tccagtcagg cagccctana 540  
 aactggggaa aaaagaaaag gacgccccan ccccagctg tgcantacg cacctcaaca 600  
 gcacagggtg gcagcaaaaa aaccacttta ctttggcaca acaaaaaact ngggggggca 660  
 accccggcac ccnangggg gtaacagga ancngggnaa cntggaacce aattnaggca 720  
 ggcccnccac ccnaatntt gctgggaaat ttttctccc cttaattntt tc 772

<210> 12  
 <211> 751  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(751)  
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 ttggctgtgt tgggtgacgtt gtcattgcaa cagaatggg gaaaggcact gttctctttg 180  
 aagtanggtg agtcctcaaa atccgtatag ttgggtgaagc cacagcactt gagccctttc 240  
 atgggtggtg tccacacttg agtgaagtct tcctgggaac cataatctt cttgatggca 300  
 ggcaactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac 360  
 agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420  
 acacttgctc tcagtcttan caccatanca gccntgaaa accaananca aagaccacna 480  
 cncggctgc gatgaagaaa tnacccnccg ttgacaaact tgcattggc tggganccac 540  
 agtggcccn aaaaattcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg 600  
 ccaacagggg ctgccccacn cncnnaacga tgancnatt gnacaagatc tncntggtct 660  
 tnatnaacnt gaaccctgcn tngtggctcc tgttcaggnc cnggcctga cttctnaann 720  
 aangaactcn gaagncccca cngganann g 751

<210> 13  
 <211> 729  
 <212> DNA  
 <213> Homo sapien



<220>  
 <221> misc\_feature  
 <222> (1)...(729)  
 <223> n = A,T,C or G

<400> 13

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accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gctcatcttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tcggggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgcag	ccggcggtgt	ggtcttagct	ctagggtttcc	tgggctgcta	tggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcatcc	tcctcctcat	cttcattgct	420
gaggttgcaa	tgctgtggtc	gccttggtgt	acaccacaat	ggctgagcac	ttcctgacgt	480
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gttggaaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaaanagt	cctttccccc	atttctgttg	caattgacaa	660
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attnaaggg						729

<210> 14  
 <211> 816  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(816)  
 <223> n = A,T,C or G

<400> 14

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tgctcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgagag	tcctgtgtct	120
ggcaggtcca	cgcagtcccc	tttgtactg	gggaaatgga	tgcgctggag	ctcgtaaaag	180
ccactcgtgt	atctttcaca	ggcagcctcg	tccgacgcgt	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcggaaactg	ggtgggctga	300
cangtgccag	agcacactgg	atggcgccct	tccatgnnan	gggccctgng	ggaaagtccc	360
tganccecan	anctgcctct	caaangcccc	accttgca	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaaggtag	ttnttcttgt	tgcccaancc	anccccntaa	acaaactctt	480
gcanatctgc	tccngggggg	tentantacc	ancgtgggaa	aagaacccca	ggcngcgaa	540
caancttggt	tggatncgaa	gcnataatct	netnttctgc	ttggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtcctcntgg	ggtgnncttg	aacctaatch	ccnntcaact	660
gggacaaggt	aantngccnt	cctttnaatt	cccnanctn	ccccctggtt	tgggggtttt	720
cncnctccta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaacctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15  
 <211> 783  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(783)  
 <223> n = A,T,C or G

&lt;400&gt; 15

ccaaggcctg	ggcaggcata	nacttgaagg	tacaacccca	ggaacccctg	gtgctgaagg	60
atgtggaaaa	cacagattgg	cgcctactgc	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaagggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtcaact	gtgctgtcca	240
ccaagcagac	agaagactac	tgcctcgcac	ccaacaangt	gggtcgctgc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcggt	tatggaggct	360
gcttgggcaa	caagaacaac	taccttcggg	aagaagagt	cattctance	tgtcnggggt	420
tgcaagggtg	gcctttgana	ngcanctctg	gggctcangc	gactttcccc	cagggccctt	480
ccatggaaa	gcgccatcca	ntgttctctg	gcacctgtca	gcccaccag	ttccgctgca	540
ncaatggctg	ctgcacnac	antttcctng	aattgtgaca	acaccccca	ntgccccaa	600
ccctcccaac	aaagcttccc	tgtnaaaaa	tacnccant	ggcttttnac	aaacncccg	660
cncctcctt	ttcccnntn	aacaaaggc	netngcctt	gaactgccc	aaccnaggaa	720
tctnccnng	aaaaantncc	ccccctggt	cctnnaance	cctccncaa	anctncccc	780
ccc						783

&lt;210&gt; 16

&lt;211&gt; 801

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(801)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 16

gccccaatc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatacaaa	60
agctgattga	agcaaccctc	tactttttgg	tcgtgagcct	tttgcttgg	gcagggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtaggggtg	agtcctcaaa	atccgtatag	ttggtgaagc	cacagcactt	gagccctttc	240
atgggtgggtg	tcacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtc	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgtctt	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngctgcga	atgaaagaaa	ntacccacgt	tgacaaactg	catggccact	ggacgacagt	540
tggcccgaan	atcttcagaa	aagggatgcc	ccatcgattg	aacacccana	tgcccactgc	600
cnacagggt	gcncncncn	gaaagaatga	gccattgaag	aaggatcctc	ntggtcttaa	660
tgaactgaaa	ccntgcatgg	tggccctgt	tcagggtctt	tggcagtga	ttctganaaa	720
aaggaaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

&lt;210&gt; 17

&lt;211&gt; 740

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(740)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 17

gtgagagcca	ggcgtccctc	tgcctgccca	ctcagtgcca	acacccggga	gctgttttgt	60
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cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg      120
agccaccatg cagtgttca gcttcattaa gaccatgatg atcctcttca atttgctcat      180
ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcacc      240
cttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgta acgtgggcta      300
cttccctcac gcagccggcg ttgtggtctt tgctcttggg ttcctgggct gctatggtgc      360
taagacggag agcaagtgtg ccctcgtgac gttctcttcc atcctcctcc tcactctcat      420
tgctgaagtt gcagctgctg tggtcgcctt ggtgtacacc acaatggctg aaccattcct      480
gacgttgctg gtantgcctg ccatcaanaa agattatggg ttcccaggaa aaattcactc      540
aantntggaa caccnccatg aaaagggctc caatttctgn tggttcccc aactataacc      600
gaattttgaa agantcnccc tacttccaaa aaaaaanant tgcctttnc cccnttctgt      660
tgcaatgaaa acntcccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa      720
caaaaaaant nnaagggttn                                     740

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&lt;210&gt; 18

&lt;211&gt; 802

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (802)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 18

```

ccgctgggtg cgctgggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca      60
caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg      120
ggatacactt tacttttagca gccaggggtga caactgagag gtgtcgaagc ttattcttct      180
gagcctctgt tagtggagga agattccggg cttcagctaa gtatgcagcg tatgtcccat      240
aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa      300
cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat      360
ggatgagtgt ggccagcgtt gcccccttgg ccgacttggc taggagcaga aattgctcct      420
ggttctgccc tgtcaccttc acttccgcac tcactactgc actgagtgtg ggggacttgg      480
gctcaggatg tccagagacg tggttccgcc cctcnctta atgacaccgn ccanncaacc      540
gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgctggc cinctacttg      600
aancttcgtc nggcccatgg aattcacnc accggaactn gtangatcca ctrnntctat      660
aaccggnccg caccgcnntt ggaactccac tcttnttnc tttacttgag ggttaaggtc      720
acccttncg ttaccttggg tccaaacctn cctgtgtcgt anantngnaa tcnggnccna      780
tnccancnc atangaagcc ng                                     802

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&lt;210&gt; 19

&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (731)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 19

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cnaagcttcc aggtnacggg ccgnaancc tgaccnagg tancanaang cagnncggg      60
gagcccaccg tcacngggng gngtctttat nggagggggc ggagccacat cnetggaent      120
cntgaccca actcccncc ncnantgca gtgatgagtg cagaactgaa ggtnacgtgg      180
caggaaccaa gancaaannc tgctccnntc caagtcggcn nagggggcgg ggctggccac      240
gncatccnt cnagtgtgn aaagcccn cctgtctact tgtttgaga acngcnnga      300

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catgcccagn gttanataac nggcngagag tnannttgcc tctcccttcc ggctgcgcgn	360
cgngtntgct tagnggacat aacctgacta cttaactgaa cccnngaate tncnccccct	420
ccactaagct cagaacaaaa aacttcgaca ccaactcantt gtcacctgnc tgctcaagta	480
aagtgtaccc catncccaat gtntgctnga ngctctgncc tgcnttlangt tcggtccctgg	540
gaagacctat caattnaagc tatgtttctg actgcctctt gctccctgna acaancnacc	600
cnncnntcca aggggggggnc ggcccccaat ccccccaacc ntnaattnan tttanccccn	660
ccccnnggcc cggcctttta cnanctcnn nnaacngggna aaacnnngc tttncccaac	720
nnaatccncc t	731

&lt;210&gt; 20

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(754)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 20

tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc	60
caacccccctc ntccaaatnn centttccgg gnggggggttc caaacccaan ttanntttgg	120
annttaaat aaatnttnt tgnggnnna anccnaatgt nangaaagt naaccanta	180
tnancttnaa tncctggaaa cngtngntt ccaaaaatnt ttaaccctta antccctccg	240
aaatngttna nggaaaaccc aanttctnt aagggtgttt gaaggntnaa tnaaaanccc	300
nnccaattgt ttttngccac gcctgaatta attggnntcc gntgttttcc nttaaaanaa	360
ggnnancccc ggttantnaa tcccccnnc cccaattata ccganttttt ttngaattgg	420
gancccnccg gaattaacgg ggnnntccc tnttgggggg cnggnncccc ccccntcggg	480
ggttngggnc aggncnnaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc	540
ccaggntgag nntnggggtt ncccccccc canggccct ctcgnanagt tggggtttgg	600
ggggcctggg atttntttc cctntttnc tcccccccc ccnggganag aggttngngt	660
tttgnctnnc ggcccnccn aagancttn ccganttnan ttaaatccnt gcctnggcga	720
agtcnttgn agggntaaan ggccccctnn cggg	754

&lt;210&gt; 21

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(755)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 21

atcancccat gacccnaac nngggaccnc tcanccggnc nnncnaccnc cggccnatca	60
nngtnagnnc actncnttn natcacnccc cncnactac gcccnananc cnacgcncta	120
nncanatncc actganngcg cgangtngan ngagaaanct nataccanag ncaccanacn	180
ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnanctc cnaagtattn	240
nncnncanac gattttcctn anccgattac centncccc tanccctcc cccccacna	300
cgaaggcnct ggncnaagg nngcgnccnc ccgctagntc cccncaagt cncncncta	360
aactcancn nattaacncc ttcntgagta tcaactcccc aatctcacc tactcaactc	420
aaaaanactn gatacaaaa atncaagcc tgnttatnac actntgactg ggtctctatt	480
ttagnngtcc ntnaanctc ctaatacttc cagtctncc tcnccaatt ccnaanggct	540
ctttcngaca gcatnttttg gtccccntt gggttcttan ngaattgcc ttentngaac	600

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gggtctctct tttccctcgg ttancctggg ttcnncgggc cagttattat ttcccntttt 660
aaattctntc cntttanttt tggcnttcna aacccccggc cttgaaaacg gccccctggt 720
aaaagggtgt tttganaaaa tttttgtttt gtccc 755

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&lt;210&gt; 22

&lt;211&gt; 849

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(849)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 22

```

tttttttttt tttttangtg tngtcgtgca ggtagagggt tactacaant gtgaanacgt 60
acgctnggar taangcgacc cgantttctag gannncctt aaaatcanac tgtgaagatn 120
atcctgnnna cgggaanggtc accggnggat nntgctaggg tgnccnctcc cannncttn 180
cataactcng nggccctgcc caccaccttc ggcggcccng ngncggggcc cgggtcattn 240
gnnttaacn cactnngcna neggtttccn ncccnncng acccnggcga tccgggggtnc 300
tctgtcttcc cctgnagnen anaaantggg ccncggnecc ctttaccct nnacaagcca 360
cngccttcta nccncngccc cccctccant nngggggact gccnanngt ccgttncnng 420
nnaccccnnn gggtnccctcg gttgtcgant cnaccgnang ccanggattc cnaaggaagg 480
tgcgttnttg gcccctaccc ttcgctncgg nncaccttc ccgacnanga nccgctcccg 540
cncnncgng cctcncctcg caacaccgc nctcntngt ncggnnnccc ccccaccgc 600
nccctcncnc ngncgnancn ctcncncc gtctcannca ccaccccgcc ccgccaggcc 660
ntcanccacn ggnngacnng nagnncntc gcncgcgcg gcgnncctt cgcncngaa 720
ctnctcngg ccantnncgc tcaancnna cnaaacgcg ctgcgcggcc cgnagcgncc 780
nccctcncga gtctcctcgn ctccnacc angnttccn cgaggacacn nnaccccgcc 840
nncangcgg 849

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&lt;210&gt; 23

&lt;211&gt; 872

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(872)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 23

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gcgcaaaacta tacttcgtc gnactcgtgc gcctcgtnc tcttttctc cgcaaccatg 60
tctgacnanc ccgattnggc ngatatcnan aagntcganc agtccaaact gantaacaca 120
cacacnncan aganaaatcc nctgccttcc anagtanacn attgaacnng agaaccangc 180
nggcgaatcg taatnaggcg tgcgcgcga atntgtnc ccgttatntn ccagctcnc 240
ctnccnacc tacntctten nagctgtcnn acccctngtn cgnaccccc naggtcggga 300
tcgggttttn nntgaccgng cnnccctcc cccctccat nacganccnc ccgcaccacc 360
nanngcncgc ncccggnct ctctgcnc ccgtctntn cccctgtngc ctggcncngn 420
accgcatga cctcgcgnn ctncnngaaa ncgnanacgt ccgggttgnn annancgctg 480
tgggnnngcg tetgncgcgt gtctcttcn ncncttcca ccatcttct tacnnggtct 540
ccncccttc tcnncacnc cctgggacgc tntcctntgc ccccttnac tccccctt 600
cgnctgncc cgncccccacc ntcatttnca nacgntctt acaannncc ggntnntcc 660
cnancngncn gtcancnag ggaagggng ggnccnntg nttgacgttg ngngangtc 720
cgaanantcc tcnctcnc cctaccct cgggcgnct ctngtntcc aacttancaa 780

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ntctcccccg ngngcncntc tcagcctenc ccccccnct ctctgcantg tncctctctc 840  
tnaccnntac gantnttcgn cncctctctt cc 872

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(815)

<223> n = A,T,C or G

<400> 24

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netgncttcc tgtgtcaaata gtatacnaaa tanatatgaa tctnatntga caaganngta	120
tctntcatta gtaacaantg tntgtccat cctgtcngan canattccca tnnattncgn	180
cgcattcncn gencantatn taatngggaa ntcnnntnnn ncaccnncat ctatcctncc	240
gncctctgac tggagagat ggatnattc tntnttgacc nacatgttca tcttggattn	300
aanancctcc cgcngnccac cgggttngng cnagccnntc ccaagacctc ctgtggaggt	360
aacctgcgtc aganncatca aacntgggaa acccgcnnc angtnnaagt ngnnncanan	420
gatcccgctc aggnntnacc atcccttcnc agcgcctcct ttngtgcctt anagnnagc	480
gtgtccnanc cncctcaaat ganacgcgc agnccanccg caattnggca caatgtcngc	540
gaacccctta gggggantna tncaaaancc caggattgtc cncncangaa atcccnanc	600
ccnccctac cennctttgg gacngtgacc aantcccga gtncagtc ggcngnctc	660
ccccaccgtt nnccttgggg ggggtgaant cngnntcanc cngncgaggn ntcgnaagga	720
accggnctn ggncgaanng ancnntcnga agnccnntc cgtataaccc cccctcncca	780
nccnactgnt agntcccccc cngggtncgg aangg	815

<210> 25

<211> 775

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(775)

<223> n = A,T,C or G

<400> 25

ccgagatgtc tcgctccgtg gccttagctg tgctcgcgt actctctctt tctggcctgg	60
aggctatcca gcgtactcca aagattcagg ttactcacg tcatccagca gagaatggaa	120
agtcaaattt cctgaattgc tatgtgtctg ggtttcatcc atccgacatt gaanttgact	180
tactgaagaa tgganagaga attgaaaaag tggagcattc agacttgtct ttcagcaagg	240
actggtcttt ctatctctg tactacactg aattcacccc cactgaaaaa gatgagtatg	300
cctgcccgtg gaaccatgtg actttgtcac agcccaagat agttaagtgg gatcgagaca	360
tgtaagcagn cncatggaa gtttgaagat gccgcatttg gattggatga attccaaatt	420
ctgcttgctt gcnttttaaat antgatatgc ntatacacc taccctttat gnccccaaat	480
tgtaggggtt acatnantgt tcnctnngga catgatcttc ctttataant cncncttcg	540
aattgccgt cncnngttn ngaatgttc cnaaccacg gttggctccc ccaggctncc	600
tcttacggaa gggcctgggc cnccttncaa ggttggggga accnaaaatt tcnctntgc	660
ccnccncca cnccttngn nncncanttt ggaacccctc cnattccctc tggcctcnna	720
nccttnncta anaaaacttn aaancgtngc naaannttn acttcccccc ttacc	775

<210> 26

<211> 820  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(820)  
 <223> n = A,T,C or G

<400> 26  
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 gaaaagggtg cggtcccat cactcctcct cccccatagc catcccagag ggggtgagtag 180  
 ccatcangcc ttcgggtggga gggagtcang gaaacaacan accacagagc anacagacca 240  
 ntgatgacca tgggcgggag cgagcctctt ccctgnaccg ggggtggcana nganagccta 300  
 nctgaggggt cacactataa acgttaacga ccnagatnan cacctgcttc aagtgcaccc 360  
 ttcctacctg acnaccagng accnnnaact gcngcctggg gacagcctcg ggancagcta 420  
 acnnagcact cacctgcccc cccatggccg tncgentccc tggctcctgnc aagggaagct 480  
 ccctgttggga attncgggga naccaaggga nccccctcct ccnctgtga aggaaaaann 540  
 gatggaattt tnccttccg gccnntcccc tcttcttta cagccccct nntactctc 600  
 tccctctntt ntcctgnnc acttttnacc ccnnnatttc ccttnattga tcggannctn 660  
 ganattccac tnnccctnc cntcnatcng naanacnaaa nactntctna cccnggggat 720  
 gggnnccctcg ntcctctct cttttctnct accnccnnt ctttgctct ccttngatca  
 780tccaaccntc gntggccntn ccccccnnn tcttttccc  
 820

<210> 27  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(818)  
 <223> n = A,T,C or G

<400> 27  
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 tgtttcttct ccgagcccca ggcagcgggtg attcagccct gcccaacctg attctgatga 120  
 ctgcggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggcgc 180  
 ctgctgagca cttccgcccc tcacctgcc cagccctgc catgagctct gggctgggtc 240  
 tccgcctcca gggttctgct cttccangca ngccancaag tggcgtggg ccacactggc 300  
 ttcttctgct cccntccctg gctctgante tctgtcttcc tgtcctgtgc angcnccttg 360  
 gatctcagtt tccctcnctc anngaactct gtttctgann tcttcantta actntgantt 420  
 tatnaccnan tggncgtnc tgcnnactt taatgggcn gaccggctaa tccctccctc 480  
 nctcccttcc anttcnnna accngctnc cntctctcc centancccg ccngggaanc 540  
 ctcctttgcc ctaccangg gccnnnaccg cccntnnctn ggggggcnnng gtnnctnnc 600  
 ctgntnnccc cncctcnnt tncctcgtec cncnncgc nngcannttc ncngtcccn 660  
 tnnctcttcn ngntcgnaa ngntcnctn tnnnnngnc ngntnntn tccctctcnc 720  
 cnnntgnang tnnntnnnc ncngnncccc nnnnnnnnn nggnntnnn tctnncngc 780  
 cccnncccc ngnattaagg cctcnnctc ccggcnc 818

<210> 28  
 <211> 731  
 <212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 28

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aggaaggcg gagggatatt gtangggatt gagggatagg agnataangg gggaggtgtg      60
tcccaacatg anggtgnngt tctcttttga angagggttg ngtttttann ccnggtgggt      120
gattnaaccc cattgtatgg agnnaaagggn tttnagggat ttttcggctc ttatcagtat      180
ntanattcct gtnaatcggg aaatnatntt tcnnncggaa aatnttgctc ccatccgnaa      240
atttctcccg ggtagtgcac nttngggggg cngccangtt tcccaggctg ctanaatcgt      300
actaaagntt naagtgggan tncaaatgaa aacctnncaac agagnatccn taccgcactg      360
tnnnttncct tcgccctntg actctgcnnng agcccaatac ccnngngnat gtcncccnng      420
nnngcgcncnc tgaaannnnnc tcgnggctnn gancatcang ggggttcgca tcaaaagcnn      480
cgtttcncat naaggcactt tngcctcacc caaccnctng ccctcnncca ttngccgctc      540
nggttcncct acgcttntng cncctnnntn ganattttnc ccgcctnggg naancctcct      600
gnaatgggta gggncctntc ttttnaccnn gnggtntact aatcnnctnc acgcntnctt      660
tctcnacccc cccctttttt caatcccanc ggcnaatggg gtctccccnn cgangggggg      720
nnncccannc c

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<210> 29

<211> 822

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(822)

<223> n = A,T,C or G

<400> 29

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actagtccag tgtggtggaa ttccattgtg ttgggggncnc ttctatgant antnttagat      60
cgctcanacc tcacancctc ccnacnangc ctataangaa nannaataga nctgtncnnt      120
atntntacnc tcatanncct cnnnacccac tccctcttaa ccctactgt gcctatngcn      180
tnnctantct ntgccgcctn cnanccaccn gtggggcncac cncnngnatt ctcnatctcc      240
tcnccatntn gcctananta ngtnccatacc ctatacctac nccaatgcta nnnctaancn      300
tccatnanti annntaacta ccaactgaent ngactttcnc atnanctcct aatttgaatc      360
tactctgact cccacngcct annnattagc anctcccccc nacnatntct caaccaaadc      420
ntcaacaacc tatctanctg ttcnccaacc nttncctcgg atccccnnac aacccccctc      480
ccaaataccc nccacctgac nctaaccncc caccatcccg gcaagccnan ggncatttan      540
ccactggaat cacnatngga naaaaaaaac ccnaactctc tancncnnat ctccctaana      600
aatnctcctn naatttactn ncantnccat caancccaac tgaaacnnaa cccctgtttt      660
tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc ccccnctnc      720
ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaaggcna anannntccg      780
canatcctat cccttanttn ggggnccctt nccnggggce cc

```

<210> 30

<211> 787

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature



&lt;222&gt; (1)...(787)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 30

cgccgcgctg	ctctggcaca	tgctctctga	atggcatcaa	aagtgatgga	ctgcccattg	60
ctagagaaga	ccttctctcc	tactgtcatt	atggagccct	gcagactgag	ggctccccct	120
gtctgcagga	tttgatgtct	gaagtcgtgg	agtgtggcct	ggagctcctc	atctacatna	180
gctggaagcc	ctggagggcc	tctctcgcca	gcctccccct	tctctccaag	ctctccangg	240
acaccagggg	ctccaggcag	cccattattc	ccagnangac	atggtgtttc	tccacgcgga	300
cccattgggg	ctgnaaggcc	agggctctct	ttgacaccat	ctctcccgct	ctgcctggca	360
ggcgtggga	tccactantt	ctanaacggn	cgccaccncg	gtgggagctc	cagcttttgt	420
tcccnttaat	gaaggttaat	tgcnegcttg	gcgtaatcat	nggtcanaac	tntttcctgt	480
gtgaaattgt	ttntccccct	ncnatteenc	ncnacatacn	aaccgggaan	cataaagtgt	540
taaagcctgg	gggtngcctn	nngaattnaac	tnaactcaat	taattgcgtt	ggctcatggc	600
ccgctttccn	ttcnggaaaa	ctgtctctcc	ctgcnttntt	gaatcgcca	ccccccnggg	660
aaaagcggtt	tgcnttttng	ggggntcctt	ccntctcccc	cctcnctaan	ccctnccgct	720
cggtcgttnc	nggtngcggg	gaangggnat	nnnctccnc	naaggggng	agnnngntat	780
ccccaaa						787

&lt;210&gt; 31

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(799)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 31

tttttttttt	tttttttggc	gatgctactg	tttaattgca	ggaggtgggg	gtgtgtgtac	60
catgtaccag	ggctattaga	agcaagaagg	aaggagggag	ggcagagcgc	cctgctgagc	120
aacaaaggac	tccctgcagc	ttctctgtct	gtctcttggc	gcaggcacat	ggggaggcct	180
cccgaggggt	ggggggccacc	agtccagggg	tgggagcact	acanggggtg	ggagtgggtg	240
gtggctggtn	cnaatggcct	gncacanatc	cctacgatct	ttgacacctg	gatttcacca	300
ggggaccttc	tgtttctcca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttctt	360
cngcanttct	ggctgttcat	ggaaagcaca	ggtgtccnat	ttnggctggg	acttgggtaca	420
tatggttccg	gcccacctct	cccntcnaan	aagtaattca	ccccccccc	ccntctnttg	480
cctgggcccct	taantaccca	caccggaact	canttantta	ttcatcttng	gntgggcttg	540
ntnatchccn	cctgaangcg	ccaagttgaa	agggcacgce	gtncccnctc	cccatagnan	600
nttttntnt	canctaatgc	ccccccnggc	aacnatccaa	tcccccccn	tggggggccc	660
agcccanggc	ccccgntcgc	ggnnnccngn	cncgnantcc	ccaggntctc	ccantcngnc	720
ccnnngcncc	ccgcacgcga	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnnncnac	780
ctcgcctccc	ccnncgng					799

&lt;210&gt; 32

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(789)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 32

tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	tttttttttt	60
ttttncnag	ggcagggtta	ttgacaacct	cncgggacac	aancaggctg	gggacaggac	120
ggcaacaggc	tccggcggcg	gcggcggcgg	ccctacctgc	ggtaccaa	ntgcagcctc	180
cgctcccgt	tgatnttct	ctgcagctgc	aggatgccnt	aaaacagggc	ctcggccntn	240
ggtgggcacc	ctgggatttn	aatttccacg	ggcacaatgc	ggtcgcanc	cctcaccacc	300
nattaggaat	agtggtnnta	cccnccnccg	ttgggncact	cccnctggaa	accacttntc	360
gcggctccgg	catctggtct	taaaccttgc	aaacnctggg	gccctctttt	tggttantnt	420
nccngccaca	atcatnactc	agactggcnc	gggctggccc	caaaaaancn	ccccaaaacc	480
ggncatgtc	ttncgggggt	tgctgcnatn	tncatcacct	cccgggcnca	ncaggncaac	540
ccaaaagttc	ttngggcccn	caaaaaanct	ccggggggnc	ccagtttcaa	caaagtcctc	600
cccttgggcc	cccaaaccct	ccccccgntt	nctgggtttg	ggaacccacg	cctctnnctt	660
tggngggcaa	gntggntccc	ccttcggggc	cccggtgggc	ccnctcttaa	ngaaaacncc	720
ntccntnnca	ccatcccccc	nngnnacgnc	tancaangna	tccctttttt	tanaaacggg	780
ccccccnccg						789

&lt;210&gt; 33

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (793)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 33

gacagaacat	ggtggatggt	ggagcacctt	tctatacgac	ttacaggaca	gcagatgggg	60
aattcatggc	tggtggagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgatgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtattt	gcaaagaaga	cgaaggcaga	gtgggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggttctga	cttttgagga	ggttgttcat	catgatcaca	300
acaangaacg	gggctcgttt	atcaccantg	aggagcagga	cgtgagcccc	cgccctgcac	360
ctctgctgct	aaacacccca	gccatccctt	ctttcaaaaag	ggatccacta	cttctagagc	420
ggncgccacc	gcggtggagc	tcagctttt	gttcccttta	gtgagggtta	attgcgcgct	480
tggcgtaatc	atggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaatttt	aaagcctggn	ggtngcctaa	tgantgaact	600
nactcacatt	aatggcttt	gcgctcactg	cccgttttcc	agtccggaaa	acctgtcctt	660
gccagctgcc	ntaatgaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgencttccc	gctttctcgc	ttcctgaant	ccttcccccc	ggtctttcgg	cttgcggnca	780
acggtatcna	cct					793

&lt;210&gt; 34

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (756)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 34

gcccgcgaccg	gcatgtacga	gcaactcaag	ggcgagtggga	accgtaaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagttc	ttctggagct	caacttcttg	120

ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtga	catactggag	180
atcgggggcc	aatggagcat	cctacgcaan	gacatcccct	ccttcgagcg	ctacatggcc	240
cagctcaaat	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttcctg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tgganggcag	ctaccncaaa	gtnttcctgg	ccnagggtaa	480
catccccgcg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcagggatg	540
aaaaatcgng	ggttgctcca	gaaaggctnc	aanaanatec	ttttcnctga	aggcccccg	600
atncnctagt	nctagaatcg	gcccgcctac	gcggtgganc	ctccaacctt	tcgttnccct	660
ttactgaggg	ttnattgccg	cccttgccgt	tatcatggtc	acncngttn	cctgtgttga	720
aattnttaac	ccccacaat	tccacgcna	catng			756

&lt;210&gt; 35

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (834)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 35

ggggatctct	anatenacct	gnatgcattg	ttgtcgggtg	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggct	gctgtnttta	agttgctcag	tctgccgtca	120
tagtcagaca	cncctctggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcngg	gctgtctgct	cggtgaactc	gatgacnang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctcct	tgggtgacctc	cccttcaaag	ttgttccggc	cttcacaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgtcactgtt	360
ggaaactgat	cccaaattgg	atgtcatcca	tcgcctctgc	tgccctgcaa	aaacttgctt	420
ggcncaaate	cgactcccn	tccttgaaag	aagccnatca	cacccccctc	cctggactcc	480
nncaangact	ctnccgctnc	cccntccnng	cagggttggg	ggcannccgg	gccntgcgc	540
ttcttcagcc	agttcacnat	nttcacagc	ccctctgcca	gctgtnttat	tccttggggg	600
ggaanccgtc	tctcccttcc	tgaannaact	ttgaccgtng	gaatagccgc	gcntcnccnt	660
acntnctggg	ccgggttcaa	antccctecn	ttgncnntcn	cctcggggcca	ttctggattt	720
ncnaacttt	tctcttcccc	cncctcncgg	ngtttggntt	tttcattngg	ccccaaactc	780
gctnttgccc	antccctgg	gggcntntan	cncctcctnt	ggtcctntng	ggcc	834

&lt;210&gt; 36

&lt;211&gt; 814

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (814)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 36

cgngcgtttt	ccngccgcgc	cccgtttcca	tgacnaaggc	tcccttcang	ttaaatacn	60
cctagnaaac	attaatgggt	tgctctacta	atacatcata	cnaaccagta	agcctgcccc	120
naacgccaac	tcaggccatt	cctaccaaag	gaagaaaggc	tggtctctcc	accccttgta	180
ggaaaggcct	gccttgtaag	acaccacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanaggtttt	gttctcatgg	ctgcccaccg	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgctctt	ttggacatca	360

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ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc 420
antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480
agggggangtc ntttncagtg gatctgccaa anantaccn tatcatcnnt gaataaaaag 540
gccctgaac ganatgcttc cancanctt taagacccat aatccctngaa ccatgggtgcc 600
cttccggctc gatccnaaag gaatgttctt gggtcccant cctccttttg ttncctacgt 660
tgtnttggac cntgtctn gn atnaccnaan tganatcccc ngaagcacc tncctctggc 720
atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcncnnaan 780
ggngaactca agaaggtctn ngaaaaacca cncn 814

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&lt;210&gt; 37

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(760)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 37

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gcatgtgct ctccctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg 60
gcgcagtgtt cgctgaagggt gttgtagtac cagcgcgga tgctctcctt gcagagtcct 120
gtgtctggca ggtccacgca atgccctttg tctactggga aatggatgct ctggagctcg 180
tcnaanccac tctgtgtattt ttcacangca gcctcctccg aagctcctcg gcagttgggg 240
gtgtctgtcac actccactaa actgtcgatn cancagccca ttgtctgcagc ggaactgggt 300
gggtctgacag gtgccagaac aacttgatn ggcttttcca tgggaagggtc tgggggaaat 360
cncctnancc caaactgcct ctcaaaggcc accttgaca ccccgacagg ctagaaatgc 420
actcttcttc ccaaaggtag ttgtcttctg tgcceaagca ncctccanca aacccaaanc 480
ttgcaaaatc tgtctcgttg gggtcattnn taccanggtt ggggaaanaa acccggcngn 540
ganccnctt gtttgaatgc naaggnaata atcctctgt cttgtctggg tggaaanagca 600
caattgaact gttaacnttg ggccnggtc cncctnggtg gtctgaaact aatcacgctc 660
actggaaaaa ggtangtgc tctcttgat tcccaaat tccctngnt tgggtnttt 720
ctcctctncc ctaaaaatcg tnttcccccc cntanggcg 760

```

&lt;210&gt; 38

&lt;211&gt; 724

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(724)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 38

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ttttttttt ttttttttt ttttttttt tttttaaaaa cccctccat tgaatgaaaa 60
cttcnnaaat tgtccaacc cctcnccaa atnccattt cgggggggg gttccaaacc 120
caaattaatt ttggantta aattaaatn tnatngggg aanaanccaa atgtnaagaa 180
aatttaacc attatnaact taaatnctn gaaaccntg gnttccaaa atttttaacc 240
cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaagggt 300
ngatttaaac ccccttnant tnttttnacc cngnctnaa ntattngnt tccggtgtt 360
tcctnttaan cntnggtaac tcccngtaat gaannccct aanccaatta aaccgaattt 420
tttttgaaat ggaaattccn ngggaattna cgggggttt tcccttttg gggccatncc 480
ccctcttctg ggggttgggn ntagggtgaa tttttnnang ncccaaaaaa nccccaana 540
aaaaaactcc caagnnttaa ttngaantc ccccttccca ggccttttg gaaaggnggg 600

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tttntggggg ccngggantt cnttccccn ttncncccc cccccnggt aaanggttat	660
ngnntttggt ttttgggccc cttnanggac cttccggatn gaaattaaat ccccggnng	720
gcg	724

&lt;210&gt; 39

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(751)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 39

tttttttttt tttttctttg ctcacattta atttttatth tgattttttt taatgctgca	60
caacacaata tttatttcat ttgtttcttt tatttcattt ttttggttg ctgctgctgt	120
tttatttatt tttactgaaa gtgagaggga acttttgttg ctttttttcc tttttctgta	180
ggccgcctta agcttttctaa atttggaaaca tctaagcaag ctgaanggaa aaggggggtt	240
cgcaaatca ctcgggggaa nggaaagggt gctttgttaa tcatgccta tgggtgggtga	300
ttaactgctt gtacaattac ntthcacttt taattaattg tgctnaangc ttttaattana	360
cttgggggtt ccttccccan accaaccctn ctgacaaaaa gtgcngccc tcaaatnatg	420
tcccggnnt cnttgaaaca cacngcngaa ngttctcatt ntccccnc caggtnaaaa	480
tgaagggtta ccatntttta cncacctcc acntggcnnt gcctgaatcc tcnaaaancn	540
cctcaancn aattctnng ccccggtcnc gcntnngtc cncccgggt cggggaantn	600
cacccccnga annnntnnc naacnaaatt ccgaaaatat tccnntcnc tcaattcccc	660
cnnagactnt cctcnnncn cncaattttc tttntntcac gaacncgnc cnnaaatgn	720
nnnnncctc cncngtccn naatcnccan c	751

&lt;210&gt; 40

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(753)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 40

gtggtatttt ctgtaagatc aggtgttcct cctcgtagg tttagaggaa acaccctcat	60
agatgaaaac cccccgaga cagcagcact gcaactgcca agcagccggg gtaggagggg	120
cgccctatgc acagctgggc ccttgagaca gcagggttc gatgtcaggc tcgatgtcaa	180
tgggtctggaa gggcggtg tacctgcgta ggggcacacc gtcagggcc accaggact	240
tctcaaagt ccaggcaacn tcgttgcgac acaccggaga ccagggtatn agcttgggt	300
cggtcataan cgcggtggcg tcgtcgttg gagctggcag ggcctccgc aggaaggcna	360
ataaaagggt cgccccgca cgttcanct cgcacttctc naanaccatg angttgggt	420
cnaaccacc accannccgg acttccttga nggaattccc aaatctcttc gntcttgggc	480
ttctnctgat gccctanctg gttgccnngn atgccaanca nccccaancc ccggggtcct	540
aaanccaccn cctctcntt tcactgtgggt tntntcccc ggacctgggt tcctctcaag	600
ggancccata tctcnaccan tactcaccnt nccccccnt gnnaccanc cttctannng	660
tcccccccg nctctgggc cntcaaanat gcttnacna cctgggtctg ccttcccccc	720
tncctatct gnaccnncn tttgtctcan tnt	753

&lt;210&gt; 41

<211> 341  
 <212> DNA  
 <213> Homo sapien

<400> 41  
 actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaagt 60  
 agtgaaccca tccttgattt atatacatat atgtttctag tattttggga gcctttccac 120  
 tcttttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt 180  
 tatagcttgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttag 240  
 tgttaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat 300  
 ttttactttt tgattaattg tgttttatat attagggtag t 341

<210> 42  
 <211> 101  
 <212> DNA  
 <213> Homo sapien

<400> 42  
 acttactgaa ttttagttctg tgetcttctt tatttagtgt tgtatcataa atactttgat 60  
 gtttcaaaca ttctaaataa ataattttca gtggcttcat a 101

<210> 43  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 43  
 acatctttgt tacagtctaa gatgtgttct taaatcacca ttccttcttg gtcttcaccc 60  
 tccagggtgg tctcacactg taattagagc tattgaggag tctttacagc aaattaagat 120  
 tcagatgcct tgctaagtct agagttctag agttatgttt cagaaagtct aagaaacca 180  
 cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat 240  
 tggatacaga acgagagtta tcttgataa ctacagagctg agtacctgcc cgggggccgc 300  
 tcgaa 305

<210> 44  
 <211> 852  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (852)  
 <223> n = A,T,C or G

<400> 44  
 acataaatat cagagaaaaag tagtctttga aatatttacg tccaggagtt ctttgttctt 60  
 gattatttgg tgtgtgtttt gggttgtgtc caaagtattg gcagcttcag ttttcatttt 120  
 ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180  
 ccagaatttc tctttttag tagtatctca tagctcggct gagcttttca taggtcatgc 240  
 tgctgttgtt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga 300  
 agacgcctc agatcggtct tcccatttta ttaatcctgg gttcttgtct gggttcaaga 360  
 ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgcttt ttggtgtggc 420  
 acttggcagg ggggtcttgc tcttttttca tatcagggtga ctctgcaaca ggaaggtgac 480  
 tgggtgttgt catggagatc tgagcccggc agaaagtgtt gctgtccaac aaatctactg 540  
 tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag 600

gctcagtttg ttcagtcctg acaatgacat tgtgtgtgga ctggaacagg tcactactgc	660
actggccggt ccacttcaga tgctgcaagt tgctgtagag gagntgcccc gccgtccctg	720
ccgcccgggt gaactcctgc aaactcatgc tgcaaagggt ctgcccgttg atgtcgaaact	780
cntggaaagg gatacaattg gcatccagct ggttgggtgtc caggagggtga tggagccact	840
cccacacctg gt	852

<210> 45  
 <211> 234  
 <212> DNA  
 <213> Homo sapien

<400> 45	
acaacagacc cttgctcgct aacgacctca tgctcatcaa gttggacgaa tccgtgtccg	60
agtctgacac catccggagc atcagcattg ctctgcagtg ccctaccgcg gggaaactctt	120
gcctcgtttc tggtctgggt ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg	180
tgaacgtgtc ggtggtgtct gaggaggtct gcagtaagct ctatgaccgc ctgt	234

<210> 46  
 <211> 590  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (590)  
 <223> n = A,T,C or G

<400> 46	
actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta	60
atttgatagc aatatttttg agattacaga gtttttagtaa ttaccaatta cacagttaaa	120
aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa	180
tgantataac taattgacaa tggaaaaatca attttaatgt gaattgcaca ttatccttta	240
aaagctttca aaanaaanaa ttattgcagt ctanttaatt caaacagtgt taaatggtat	300
caggataaan aactgaaggg canaaaagaat taattttcac ttcatgtaac ncacccanat	360
ttacaatggc ttaaattgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc	420
tggtctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag	480
ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct	540
gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt	590

<210> 47  
 <211> 774  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (774)  
 <223> n = A,T,C or G

<400> 47	
acaagggggc ataataagg agtggggana gatttttaaag aaggaaaaaa aacgaggccc	60
tgaacagaat ttctctgnac aacgggggctt caaaataatt ttcttgggga ggttcaagac	120
gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg	180
cattacagac gggactctgg gaggaaggat aaacagaaaag gggacaaaag ctaatcccaa	240
aacatcaaag aaaggaagggt ggcgtcatat ctcccagcct acacagttct ccagggtctt	300

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cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctccctgtgtg 360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgtgat cctgcgtggc 420
ccacactcct tgaacacaca tccccagggt atattcctgg acatggctga acctcctatt 480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc 540
acggcatggg aagcctttct gacttgctg attactccag catcttgga caatccctga 600
ttccccactc cttagaggca agatagggtg gttaagagta gggctggacc acttgagacc 660
aggctgctgg cttcaaattn tggctcatt acgagctatg ggaccttggg caagtnatct 720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

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&lt;210&gt; 48

&lt;211&gt; 124

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(124)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 48

```

canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt 60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact 120
tggt 124

```

&lt;210&gt; 49

&lt;211&gt; 147

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(147)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 49

```

gccgatgcta ctattttatt gcaggagggt ggggtgtttt tattattctc tcaacagctt 60
tgtggctaca ggtgggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt 120
ttagggcacc catatcccaa gcantgt 147

```

&lt;210&gt; 50

&lt;211&gt; 107

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 50

```

acattaaatt aataaaagga ctgttggggt tctgctaaaa cacatggctt gatattattgc 60
atcggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

```

&lt;210&gt; 51

&lt;211&gt; 204

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 51

```

gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgacagg 60

```



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cggggaaggaa aggcagagaa gtgacaccgt cagggggaaa tgacagaaag gaaaatcaag      120
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttgcca      180
cctccctttt gggaccagca atgt      204

```

&lt;210&gt; 52

&lt;211&gt; 491

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(491)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 52

```

acaaagataa catttatctt ataacaaaaa tttgatagtt ttaaagggtta gtattgtgta      60
gggtattttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca      120
ccatcagaca ggtttttaaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa      180
aaaacttctt gtatcaattt cttttgttca aaatgactga ctttaantatt tttaaatatt      240
tcanaaacac ttcctcaaaa attttcaana tggtagcttt canatgtgcc ctcagtccca      300
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc      360
atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat      420
caattttatt tggataacaa agggctctcca aatttatattg aaaaataaat ccaagttaat      480
atcactcttg t      491

```

&lt;210&gt; 53

&lt;211&gt; 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(484)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 53

```

acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga      60
gtattaacag ttgctgaagt ttggatattt tatgcagcat tttctttttg ctttgataac      120
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct      180
caatcaaate tctacataac actatagtaa ttaaaacgtt aaaaaaaagt gttgaaatct      240
gcactagtat anaccgctcc tgtcaggata anactgctt ggaacagaaa gggaaaaanc      300
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct      360
aatgattggc aggtcnggta aatnccaaa catattccaa ctcaacactt cttttccncg      420
tancctgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc      480
cant      484

```

&lt;210&gt; 54

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 54

```

actaaacctc gtgcttgatga actccatata gaaaacgggtg ccacccctga acacggctgg      60
ccactgggta tactgctgac aaccgcaaca aaaaaaacac aaatccttgg cactggctag      120
tctatgtcct ctcaagtgcc tttttgtttg t      151

```

<210> 55  
<211> 91  
<212> DNA  
<213> Homo sapien

<400> 55  
acctggcttg tctccgggtg gttcccggtg cccccacgg tccccagaac ggacactttc 60  
gccctccagt ggatactcga gccaaagtgg t 91

<210> 56  
<211> 133  
<212> DNA  
<213> Homo sapien

<400> 56  
ggcggatgtg cgttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60  
tggatttttg gtatctgtgg gttgggggga cggctccagga accaataccc catggatacc 120  
aagggacaac tgt 133

<210> 57  
<211> 147  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(147)  
<223> n = A,T,C or G

<400> 57  
actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60  
gactgggagc tgagcccttc cctttgcgcc tgcctcagag gattgttgcc gacntgcana 120  
tctcantggg ctggatncat gcagggt 147

<210> 58  
<211> 198  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(198)  
<223> n = A,T,C or G

<400> 58  
acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60  
tgattacata catttatcct ttaaaaaaga tgtaaatctt aatttttatg ccatctatta 120  
atttaccat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180  
ttgacttcta agtttggt 198

<210> 59  
<211> 330  
<212> DNA  
<213> Homo sapien

&lt;400&gt; 59

acaacaaatg ggttgtgagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat	60
ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt	120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa	180
tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagaccag	240
cagaaggaaat ctattttatac acatggatct ccgtctgtgc tcaaaatacc taatgatatt	300
tttcgtcttt attggacttc tttgaagagt	330

&lt;210&gt; 60

&lt;211&gt; 175

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 60

accgtgggtg cttctacat tcttgacggc tccttcacca acatctgggt ctacttcggc	60
gtcgtgggtc cttctctctt catcctcctc cagctgggtg tgctcatcga ctttgccgac	120
tcctggaacc agcggagggt gggcaaggcc gaggagtgcg attcccgtgc ctgggt	175

&lt;210&gt; 61

&lt;211&gt; 154

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 61

accccacttt tcctcctgtg agcagtcctgg acttctcact gctacatgat gagggtgagt	60
ggttggtgct cttcaacagt atcctccctt tccggatct gctgagccgg acagcagtgc	120
tggaactgcac agccccgggg ctccacattg ctgt	154

&lt;210&gt; 62

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 62

cgctcgagcc ctatagttag tcgtattaga	30
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&lt;210&gt; 63

&lt;211&gt; 89

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 63

acaagtcatt tcagcacct ttgctcttca aaactgacca tcttttatat ttaatgcttc	60
ctgtatgaat aaaaatgggt atgtcaagt	89

&lt;210&gt; 64

&lt;211&gt; 97

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 64

accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag	60
aatcagtgc tccaggattg gtccttggat ctgggggt	97

<210> 65  
 <211> 377  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (377)  
 <223> n = A,T,C or G

<400> 65  
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccccct ttgatggca 60  
 gcatggcgtc ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc 120  
 ccaacctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180  
 tgggtcataa natgaaatcc caanggggac agaggtcagt agagggaagct caatgagaaa 240  
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300  
 tgggggtgaa ctaccccan gaggaatcat gctggggcga tgcaanggtg ccaacaggag 360  
 gggcgggagg agcatgt 377

<210> 66  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 66  
 acgcctttcc ctccagaattc agggaagaga ctgtcgctg ccttccctccg ttgttgctg 60  
 agaaccctgt tggcccttcc caccatattc accctcgctc catctttgaa ctcaaacacg 120  
 aggaactaac tgcacctgg tctctcccc agtccccagt tcacctcca tccctcacct 180  
 tctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240  
 ttatatattt ttttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300  
 tgttt 305

<210> 67  
 <211> 385  
 <212> DNA  
 <213> Homo sapien

<400> 67  
 actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60  
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggt ctgagagttc 120  
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180  
 tgtgctgtgc tggagattca cttttgagag agttctctc tgagacctga tctttagagg 240  
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300  
 cctctccag gggccagcc tggccacacc tgcttacagg gcactctcag atgcccatc 360  
 catagtttct gtgctagtgg accgt 385

<210> 68  
 <211> 73  
 <212> DNA  
 <213> Homo sapien

<400> 68  
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaa tgaaaaataa 60  
 gtttttttaa tgg 73

<210> 69  
<211> 536  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(536)  
<223> n = A,T,C or G

<400> 69  
actagtcacg tgtgggtggaa ttccattgtg ttggggggctc tcaccctcct ctccctgcagc 60  
tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120  
cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180  
cccggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240  
cgccatcagc gagtataaca aggccacca agatgactac tacagacgtc cgctgcgggt 300  
actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagagggtgg 360  
ccgaaccata tgtaccaagt cccagcccaa ctgggacacc tgtgccttcc atgaacagcc 420  
agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagtccct ggggagaaca 480  
gaangtcctt gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70  
<211> 477  
<212> DNA  
<213> Homo sapien

<400> 70  
atgaccctta acagggggcc tctcagccct cctaattgacc tccggcctag ccatgtgatt 60  
tcacttccac tccataacgc tcctcatact aggcctacta accaacacac taaccatata 120  
ccaatgatgg cgcgatgtaa cagagaaaag cacataccaa ggccaccaca caccacctgt 180  
ccaaaaaggc cttcgatagc ggataatcct atttattacc tcagaagttt ttttcttcgc 240  
agggattttt ctgagccttt taccactcca gcctagcccc tccccccaa ctaggagggc 300  
actggccccc aacaggcacc accccgctaa atcccctaga agtcccactc ctaaacacat 360  
ccgtattact cgcacagga gtatcaatca cctgagctca ccatagtcta atagaaaaca 420  
accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt 477

<210> 71  
<211> 533  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(533)  
<223> n = A,T,C or G

<400> 71  
agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60  
aggatattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattgggtta 120  
tgtgatttta gtgggtattt tggcaccctt atatatgttt tccaaacttt cagcagtgat 180  
attattttcca taacttaaaa agtgagtgtt aaaaagaaaa tctccagcaa gcattctcatt 240  
taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300  
aaatagggtg gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360  
agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420  
cttcgtaatt ttggagtang aggttccttc ctcaattttg tattttttaa aagtacatgg 480  
taaaaaaaaa aattcacaac agtatataag gctgtaaaaa gaagaattct gcc 533

<210> 72  
 <211> 511  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(511)  
 <223> n = A,T,C or G

<400> 72  
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60  
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120  
 aagccgcagg atgtctacac tatancaggc gctatattggg ttggctggag gagctgtgga 180  
 aaacatggan agattgggtgc tgganategc cgtggctatt cctcattgtt attaccanagt 240  
 gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300  
 cacatgagaa ctgaaatggc ccaaaccagc aaagaaagcc caactagatc ctcagaanac 360  
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420  
 atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggtg atgatggcna 480  
 aaatacaccc cctcttgaag naccnggagg a 511

<210> 73  
 <211> 499  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(499)  
 <223> n = A,T,C or G

<400> 73  
 cagtgccagc actggtgcca gtaccagtac caataacagt gccagtgccca gtgccagcac 60  
 cagtgggtggc ttcagtgtct gtgccagcct gaccgccact ctcacatttg ggctcttcgc 120  
 tggccttggg ggagctgggt ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180  
 caagtgaagt tttagatatt gttaatcctg ccagtcttct tcttcaagcc aggggtgcac 240  
 ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300  
 ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggc cgccgctcg 360  
 antctagagg gcccggttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420  
 catctgttgt ttgccctccc cccgntgcct tccttgacct tggaaagtgc cactcccact 480  
 gtcctttcct aantaaaat 499

<210> 74  
 <211> 537  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(537)  
 <223> n = A,T,C or G

<400> 74  
 ttctcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat 60

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ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact 120
tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180
cattgtatgc atggaaacat ggaggaacag tattacagtg tcctaccact ctaatcaaga 240
aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300
ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc 360
cagtttgctt gatataattg ttgatattaa gattcttgac ttatatattg aatgggttct 420
actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480
tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccgt 537

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&lt;210&gt; 75

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(467)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 75

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caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60
tgcataattac acgtacctcc tcctgtctct caagtagtgt ggtctatatt gccatcatca 120
cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
tggcacaagg aggccatctt ttctcatcg gttattgtcc ctagaagcgt cttctgagga 240
tctagtggg ctttctttct gggtttgggc catttcantt ctcagtgtg tactattcta 300
tcattattgt ataacgggtt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420
ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tcctgn 467

```

&lt;210&gt; 76

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(400)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 76

```

aagctgacag cattcggggc gagatgtctc gctccgtggc cttagctgtg ctgcgctac 60
tctctcttct tggcctggag gctatccagc gtactccaaa gattcaggtt tactcacgtc 120
atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg ttcatccat 180
ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagtg gagcattcag 240
acttgtcttt cagcaaggac tgggtcttct atctcttgta ctacactgaa ttcaccccca 300
ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
ttnagtggga teganacatg taagcagcan catgggaggt 400

```

&lt;210&gt; 77

&lt;211&gt; 248

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 77

```

ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcactt 60

```

```

ccagctgccc cggcggggga tgcgaggttc ggagcaccct tgcccggctg tgattgctgc      120
caggcactgt tcattctcagc tttctgtcc ctttgtcccc ggcaagcgct tctgctgaaa      180
gttcatatct ggagcctgat gtcttaacga ataaagggtcc catgctccac ccgaaaaaaa      240
aaaaaaaaa                                     248

```

```

<210> 78
<211> 201
<212> DNA
<213> Homo sapien

```

```

<400> 78
actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca      60
tcacccagac cccgccctgc ccgtgcccac cgctgctgct aacgacagta tgatgcttac      120
tctgtacttc ggaaactatt tttatgtaat taatgtatgc tttctgttt ataatgcct      180
gatttaaaaa aaaaaaaaaa a                                     201

```

```

<210> 79
<211> 552
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (552)
<223> n = A,T,C or G

```

```

<400> 79
tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg      60
tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt      120
cctctttcct ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag      180
tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt      240
atgcaagtta gtaattactc agggttaact aaattacttt aatatgctgt tgaacctact      300
ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga      360
taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta      420
ttcccaggaa tatgggggtc atttatgaat antacccggg anagaagttt tgantnaaac      480
cngttttggt taatacgtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa      540
aaaaaaaaa aa                                     552

```

```

<210> 80
<211> 476
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (476)
<223> n = A,T,C or G

```

```

<400> 80
acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga      60
ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccttggcct      120
cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt      180
gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcaacta      240
agggttaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt accttcatac      300
tcttctaagt cctcttccag cctcactttg agtcctcctt gggggttgat aggaantntc      360

```



tcttggcttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420  
gctgaaaaaa ttaaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81

<211> 232

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(232)

<223> n = A,T,C or G

<400> 81

tttttttttg tatgccttcn ctgtggngtt attgttgctg ccacctgga ggagcccagt 60  
ttcttctgta tctttctttt ctgggggatc ttcttggtc tgccttcca tttccagcct 120  
ctcatcccca tcttgcaact ttgctagggt tggaggcgt ttcttggtg cccctcagag 180  
actcagtcag cgggaataag tcttaggggt ggggggtgtg gcaagccggc ct 232

<210> 82

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 82

aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60  
agtaccagta ccaataacat gccagtgccg gtgccagcac cagtgggtggc ttcagtgtgt 120  
gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggg ggagctgggt 180  
ccagcaccag tggcagctct ggtgctgtgt gtttctccta caagtgagat tttagatatt 240  
gttaatcttg ccagctctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300  
agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360  
ccatttcaaa aaaaaaaaaa aaa 383

<210> 83

<211> 494

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(494)

<223> n = A,T,C or G

<400> 83

accgaattgg gaccgctggc ttataagcga tcatgtcttc cagtattacc tcaacgagca 60  
gggagatcga gtctatacgc tgaagaaatt tgaccgatg ggacaacaga cctgtctcagc 120  
ccatcctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180  
acgcttcaag gtgctcatga cccagcaacc gcgccctgtc ctctgagggt ccttaaaactg 240  
atgtcttttc tggccactgt taccctctcg agactcctga accaaaactct tcggactgtg 300  
agccctgatg cctttttgac agccatactc tttggentcc agtctctcgt ggcgattgat 360

```

tatgcttggtg tgaggcaatc atggtggcat caccatnaa gggaacacat ttganttttt 420
tttcncatat tttaaattac naccagaata ntccagaata aatgaattga aaaactctta 480
aaaaaaaaaa aaaa 494

```

<210> 84

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 84

```

gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca 60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120
gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg 180
gcacaccctc ctggggccca ggccggcacc tgcgtctccc agtatgccaa ctggctggtg 240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg 300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
agcgtnccg cctcatccgg 380

```

<210> 85

<211> 481

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(481)

<223> n = A,T,C or G

<400> 85

```

gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggctctcgc ttcataccgc 60
tnccatcgtc atactgtagg ttgcccacca cctcctgcat cttggggcgg ctaatatcca 120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tgggtctgtc ttccgctcgg 180
tgtgaaagga tctccagaag gagtgtcga tcttcccac acttttgatg actttattga 240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc 300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac 360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggngaa 420
aaagaacacc tcttggaagt gctngccgct cctcgtccnt tgggtggnngc gcntnccctt 480
t 481

```

<210> 86

<211> 472

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(472)

<223> n = A,T,C or G

<400> 86

```

aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt      60
acttgaaaaa gcaacttnaa gcctggacac tggattataa attcacaata tgcaacactt      120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg      180
ccctatcac  acctgttaa  agggcgctaa gcatttttga ttcaacatct ttttttttga      240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagccaat tcactttctt      300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg      360
atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga      420
tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg              472

```

&lt;210&gt; 87

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(413)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 87

```

agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaatth tgtgtgctg      60
tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttga aaagcttatg      120
cctcttttgt atctatatct gtgaaagtth taatgatctg ccataatgtc ttggggacct      180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg      300
ggggacaaag aaaagcnaaa ctgaacatna gaaacaatth cctggtgaga aattncataa      360
acagaaattg ggtngtatat tgaaanann gcatctnaa acgttttttt ttt              413

```

&lt;210&gt; 88

&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(448)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 88

```

cgcagcgggt cctctctatc tagctccagc ctctcgctg cccactccc cgcgtcccgc      60
gtcctagccn accatggccg ggccctgctg cgcccgctg ctctgctgg ccactctggc      120
cgtggccctg gccgtgagcc ccgcggcccg ctccagctcc ggcaagccgc cgcgcctggt      180
gggaggccca tggaccccg gtggaagaag aagggtgctg gcgtgcactg gactttgccg      240
tcggcnanta caacaaacc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc      300
cccaancaaa ttgttactng gggtaanata ttcttggaa ttgaacctgg gccaaacnng      360
tttaccagaa ccnagccaat tngaacaatt nccctcccat aacagccctt tttaaaaagg      420
gaancantcc tgnctctttc caaattht              448

```

&lt;210&gt; 89

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(463)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 89

gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca	60
gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaatttagc	120
agaggtctag gtctgcatat cagcagacag ttgtccgtg tattttgtag ccttgaagtt	180
ctcagtgaca agttnnttct gatgcgaagt tctnatcca gtgttttagt cctttgcac	240
tttnatgtn agacttgctt ctntnaaatt gcttttgnt tctgcaggta ctatctgtgg	300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn	360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn	420
aattcnnana anttcagntn tcatacaaca naacngganc ccc	463

&lt;210&gt; 90

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(400)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 90

agggattgaa ggtctnttnt actgtcggac tgttcancca ccaactctac aagttgctgt	60
cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaacaaat	120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttccact	180
tcctttgtta agacttcac tcgttaaagtc ttaagttttg tagaaaggaa tttaattgct	240
cgttctctaa caatgtcctc tccttgaagt atttggctga acaaccacc tnaagtcct	300
ttgtgcatcc attttaaata tacttaatag ggcattggtt cactagggtta aattctgcaa	360
gagtcactctg tctgcaaaag ttgcgttagt atatctgcc	400

&lt;210&gt; 91

&lt;211&gt; 480

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(480)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 91

gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac	120
atgcctcttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nncgctctt	180
tgtggaaaaa ctggcacttg nctggaaacta gcaagacatc acttacaaat tcaccacga	240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt	300
tgtcaatact aaccgctgg tttgcctcca tcacatttgt gatctgtagc tctggataca	360
tctcctgaca gtactgaaga acttctctt ttgtttcaaa agcaactctt ggtgcctgtt	420
ngatcaggtt cccatttccc agtccgaatg ttcacatggc atatnttact tcccacaaaa	480

&lt;210&gt; 92

&lt;211&gt; 477

&lt;212&gt; DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

atacagccca	natcccacca	cgaagatgcg	cttgttgact	gagaacctga	tgcggtcact	60
ggctccgctg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgcactcctt	120
cccacgcagg	cagcagcggg	gccggccaat	gaactccact	cgtggcttgg	ggttgacggt	180
taantgcagg	aagaggctga	ccacctcgcg	gtccaccagg	atgcccgaact	gtgcgggacc	240
tgcagcgaaa	ctcctcgatg	gtcatgagcg	ggaagcgaat	gangcccagg	gccttgccca	300
gaaccttccg	cctgttctct	ggcgccacct	gcagctgctg	ccgctnacac	tcggcctcgg	360
accagcggac	aaacggcggt	gaacagccgc	acctcacgga	tgcccantgt	gtcgcgctcc	420
aggaacggcn	ccagcgtgtc	caggtcaatg	tcggtgaanc	ctccgcgggt	aatggcg	477

<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 93

gaacggctgg	accttgcttc	gcattgtgct	gctggcagga	ataccttggc	aagcagctcc	60
agtccgagca	gccccagacc	gctgccgccc	gaagctaagc	ctgcctctgg	ccttccccctc	120
cgctccaatg	cagaaccant	agtgggagca	ctgtgttttag	agttaagagt	gaacactgtg	180
tgattttact	tgggaatttc	ctctgttata	tagcttttcc	caatgcta	ttccaaacaa	240
caacaacaaa	ataacatgtt	tgctgtttna	gttggtataaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgttaca	tatactgctt	gcaanttctg	tatttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

<210> 94

<211> 495

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(495)

<223> n = A,T,C or G

<400> 94

ccctttgagg	ggttagggc	cagttcccag	tggaagaaac	aggccaggag	aantgcgtgc	60
cgagctgang	cagatttccc	acagtgaccc	cagagccctg	ggctatagtc	tctgacctct	120
ccaaggaaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	180
gaaggcccca	ttccggggct	gttccccgag	gaggaaggga	aggggctctg	tgtgcccccc	240
acgaggaana	ggccttgant	cctgggatca	nacaccctt	cacgtgtatc	cccacacaaa	300
tgcaagctca	ccaaggctcc	ctctcagtc	cttccctaca	ccctgaacgg	ncactggccc	360
acaccacccc	agancancca	cccgccatgg	ggaatgttct	caaggaatcg	cngggcaacg	420
tggactctng	tcccnnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480

aaaaaaaaana aaaaaa

495

&lt;210&gt; 95

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(472)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 95

ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgccgag	agcggacttt	gtaattggtg	gagaataact	gctgaatttt	120
tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctattnnact	180
tattttattat	cttctgaaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	240
atgatgaaaa	gcaatagata	tatattcttt	tattatgtnn	aattatgatt	gccattatta	300
atcggaacaa	tgtggagtgt	atgttctttt	cacagtaata	tatgcctttt	gtaacttcac	360
ttggttattt	tattgtaaat	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	420
tttanttcan	taatttcttt	ccttggtttac	gttaattttg	aaaagaatgc	at	472

&lt;210&gt; 96

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(476)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 96

ctgaagcatt	tcttcaaact	tntctacttt	tgtcattgat	acctgtagta	agttgacaat	60
gtgggtgaaat	ttcaaaatta	tatgtaactt	ctactagttt	tactttctcc	cccaagtctt	120
ttttaactca	tgattttttac	acacacaatc	cagaacttat	tatatagcct	ctaagtcttt	180
attcttcaca	gtagatgatg	aaagagtctt	ccagtgtctt	gngcanaatg	ttctagntat	240
agctggatac	atacngtggg	agttctataa	actcatacct	cagtgggact	naaccaaata	300
tgtgttagtc	tcaattccta	ccacactgag	ggagcctccc	aaatcactat	attcttatct	360
gcaggtactc	ctccagaaaa	acngacaggg	caggcttgca	tgaaaaagtn	acatctgcgt	420
tacaaagtct	atcttctcta	nangtctgtn	aaggacaat	ttaatcttct	agcttt	476

&lt;210&gt; 97

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(479)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 97

actctttcta	atgctgatat	gatcttgagt	ataagaatgc	atatgtcact	agaatggata	60
aaataatgct	gcaaaactta	tgttcttatg	caaaatggaa	cgctaataga	acacagctta	120

caatcgcaaa tcaaaactca caagtgtctca tctgtttag atttagtgta ataagactta	180
gattgtgtct cttcggatat gattgtttct canatcttgg gcaatnttcc ttagtcaaat	240
caggctacta gaattctgtt attgatata tgagagcatg aaatttttaa naatacactt	300
gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat	360
ntnnttttta natcaaagta ttttgtgttt ggaantgttn aaatgaaatc tgaatgtggg	420
ttcnatctta ttttttcccn gacnactant tnccttttta gggncatttc tganccatc	479

&lt;210&gt; 98

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 98

agtgaactgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta	60
tgctagtctc tgctacttat tcgtactata atgcagactg gaggggacca aaaaggggca	120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga	180
agtgaattcag tttcctctac ggatgagaga ctggctcaag aatatectca tgcagcttta	240
tgaagccact ctgaacacgc tgggttatcta gatgagaaca gagaaataaa gtcagaaaat	300
ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct ctttaaggact	360
ttaagaaaaa ctaccacatg ttgtgtatcc tgggtgccggc cgtttatgaa ctgaccaccc	420
tttgggaataa tcttgacgct cctgaacttg ctctctgcg a	461

&lt;210&gt; 99

&lt;211&gt; 171

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 99

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&lt;210&gt; 100

&lt;211&gt; 269

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 100

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cgagagatac gcaggtgcag gtggccgcc	269

&lt;210&gt; 101

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 101

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<212> DNA  
<213> Homo sapien

<400> 102  
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<213> Homo sapien

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<211> 578  
<212> DNA  
<213> Homo sapien

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<210> 105  
<211> 538  
<212> DNA



&lt;213&gt; Homo sapien

&lt;400&gt; 105

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&lt;210&gt; 106

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 106

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&lt;210&gt; 107

&lt;211&gt; 1621

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 107

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&lt;210&gt; 108

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 108

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20     25     30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35     40     45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50     55     60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65     70     75     80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85     90     95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100    105    110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115    120    125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130    135    140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145    150    155    160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165    170    175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180    185    190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195    200    205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210    215    220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225    230    235    240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245    250    255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
260    265    270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
275    280    285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
290    295    300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
305    310    315    320
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala

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	340		345		350										
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	355		360		365										
Ser	Asp	Lys	Ile	Ile	Glu	Ser	Asn	Lys	Val	Lys	Ala	Ser	Leu		
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&lt;210&gt; 109

&lt;211&gt; 1524

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 109

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&lt;210&gt; 110

&lt;211&gt; 3410

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 110

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&lt;210&gt; 111

&lt;211&gt; 1289

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 111

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tgaagatctt cgggccactg tcgtccagtg ccatgcagtt tgtcaacgtg ggctacttcc      300
tcatcgagc cggcggttgtg gtctttgtct ttggtttcct gggctgctat ggtgctaaga      360
ctgagagcaa gtgtgccctc gtgacgttct tcttcatect cctcctcacc ttcattgctg      420
aggttgagc tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt      480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt      540
ggaacaccac catgaaaagg ctcaagtgcg gtggcttcac caactatacg gattttgagg      600
actcacccta cttcaaagag aacagtgcct ttccccatt ctgttgcaat gacaacgtca      660
ccaacacagc caatgaaacc tgcaccaagc aaaagggtca cgacaaaaaa gtagagggtt      720
gcttcaatca gcttttgtat gacatccgaa ctaatgcagt caccgtgggt ggtgtggcag      780
ctggaattgg gggcctcgag ctggctgcc aagattgtgt catgtatctg tactgcaatc      840
tacaataagt ccacttctgc ctctgccact actgctgcc catgggaact gtgaagaggc      900
accctggcaa gcagcagtg tggggggagg ggacaggatc taacaatgtc acttgggcca      960
gaatggacct gccctttctg ctccagactt ggggctagat agggaccact ccttttagcg     1020
atgcctgact ttccttccat tgggtgggtg atgggtgggg ggcattccag agcctctaag     1080
gtagccagtt ctgttgccca ttccccagt ctattaaacc cttgatatgc cccctaggcc     1140
tagtggtagt cccagtgtc tactggggga tgagagaaaag gcattttata gcctgggcat     1200
aagtgaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc     1260
tgttacaatg ttaaaaaaaaa aaaaaaaaaa

```

1289

&lt;210&gt; 112

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 112

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1          5          10          15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20          25          30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35          40          45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50          55          60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65          70          75          80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85          90          95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100          105          110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
115          120          125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130          135          140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145          150          155          160
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165          170          175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
180          185          190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu

```

```

      195              200              205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
  210              215              220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
225              230              235              240
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
      245              250              255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
      260              265              270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
      275              280              285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
      290              295              300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
305              310              315

```

```

<210> 113
<211> 553
<212> PRT
<213> Homo sapien

```

```

      <400> 113
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
  1              5              10              15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
      20              25              30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
      35              40              45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
      50              55              60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
      65              70              75              80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
      85              90              95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
      100              105              110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
      115              120              125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
      130              135              140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
      145              150              155              160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
      165              170              175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
      180              185              190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
      195              200              205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
      210              215              220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
      225              230              235              240
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
      245              250              255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg

```

```

      260      265      270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
      275      280      285
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
      290      295      300
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
      305      310      315      320
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
      325      330      335
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
      340      345      350
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
      355      360      365
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
      370      375      380
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
      385      390      395      400
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
      405      410      415
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
      420      425      430
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
      435      440      445
Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
      450      455      460
Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
      465      470      475      480
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
      485      490      495
Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
      500      505      510
Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
      515      520      525
Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
      530      535      540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala
      545      550

```

&lt;210&gt; 114

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 114

```

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
  1           5           10           15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
      20           25           30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
      35           40           45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
      50           55           60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
      65           70           75           80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile

```

```
<210> 115
<211> 366
<212> DNA
<213> Homo sapien
```

```
<210> 116
<211> 282
<212> DNA
<213> Homo sapien
```

<400> 116

<210> 117  
<211> 305



<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(305)  
<223> n = A,T,C or G

<400> 117  
acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca 60  
tatttatcct ccttcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120  
aataaggcaa aatatatgaa acaacagggtc tcgagatatt ggaaatcagt caatgaagga 180  
tactgatccc tgatcactgt cctaattgcag gatgtgggaa acagatgagg tcacctctgt 240  
gactgccccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300  
tgggt 305

<210> 118  
<211> 71  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(71)  
<223> n = A,T,C or G

<400> 118  
accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa 60  
aantcctggg t 71

<210> 119  
<211> 212  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(212)  
<223> n = A,T,C or G

<400> 119  
actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca 60  
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120  
agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctcactaanc ggaattaant 180  
aatggantca aganactccc aggcctcagc gt 212

<210> 120  
<211> 90  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(90)  
<223> n = A,T,C or G

<400> 120  
 actcggttgca natcaggggc cccccagagt caccggttgca ggagtccttc tggctcttgcc 60  
 ctccgccggc gcagaacatg ctgggggtggt 90

<210> 121  
 <211> 218  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(218)  
 <223> n = A,T,C or G

<400> 121  
 tgtancgtga anacgacaga nagggttgtc aaaaatggag aanccttgaa gtcattttga 60  
 gaataagatt tgctaaaaga tttggggcta aaacatgggtt attgggagac atttctgaag 120  
 atatncangt aaattangga atgaattcat gggtcttttg ggaattcctt tacgatngcc 180  
 agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122  
 <211> 171  
 <212> DNA  
 <213> Homo sapien

<400> 122  
 taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60  
 catttgtag ctcatggaac aggaagtcgg atggtggggc atcttcagtg ctgcatgagt 120  
 caccaccccg gcggggtcac ctgtgccaca ggccctggt gacagtgcgg t 171

<210> 123  
 <211> 76  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(76)  
 <223> n = A,T,C or G

<400> 123  
 tgtagcgtga agacnacaga atggtgtgtg ctgtgctatc caggaacaca ttattatca 60  
 ttatcaanta ttgtgt 76

<210> 124  
 <211> 131  
 <212> DNA  
 <213> Homo sapien

<400> 124  
 acctttcccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt 60  
 caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120  
 ttaagatttg t 131

<210> 125  
 <211> 432  
 <212> DNA  
 <213> Homo sapien

<400> 125  
 actttatcta ctggctatga aatagatggg ggaaaattgc gttaccaact ataccactgg 60  
 cttgaaaaag aggtgatagc tcttcagagg acttgtgact tttgtcaga tgctgaagaa 120  
 ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat 180  
 ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240  
 ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc 300  
 catggtgggg gtcttgcac tgtaagaatg gaattgattt tgcttttgca agaattctcag 360  
 caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccct agtgcctctc 420  
 ctctttgctt gt 432

<210> 126  
 <211> 112  
 <212> DNA  
 <213> Homo sapien

<400> 126  
 acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60  
 agtaagaatg atatttcccc ccagggatca ccaaataatt ataaaaattt gt 112

<210> 127  
 <211> 54  
 <212> DNA  
 <213> Homo sapien

<400> 127  
 accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128  
 <211> 323  
 <212> DNA  
 <213> Homo sapien

<400> 128  
 acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60  
 acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgtca 120  
 ttctctctga agtctaggtt acccattttg gggaccatt ataggcaata aacacagttc 180  
 ccaaagcatt tggacagttt cttgttggtt tttagaatgg ttttcctttt tcttagcctt 240  
 ttcttgcaaa aggtctactc agtcccttgc ttgtcagtg gactgggctc cccagggcct 300  
 aggtctgcctt cttttccatg tcc 323

<210> 129  
 <211> 192  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (192)  
 <223> n = A,T,C or G

&lt;400&gt; 129

```
acatacatgt gtgtatatatt ttaaatatca cttttgtatc actctgactt ttttagcatatc 60
tgaaaacaca ctaacataat ttntgtgaac catgacgaga tacaacccaa atcattcatc 120
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180
gataaacaaa gt 192
```

&lt;210&gt; 130

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(362)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 130

```
ccctttttta tggaaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60
tataatgacg caacaaaaag gtgctgttta gtccatgggt tcagtttatg cccctgacaa 120
gtttccattg tgttttgccg atcttctggc taatcgtggg atcctccatg ttattagtaa 180
ttctgtattc cattttgta acgcctggta gatgtaacct gctangaggc taactttata 240
cttatttaaa agctcttatt ttgtggatcat taaaatggca atttatgtgc agcactttat 300
tgcagcagga agcacgtgtg gggtgggtgt aaagctcttt gctaatttta aaaagtaatg 360
gg 362
```

&lt;210&gt; 131

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(332)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 131

```
ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt tccccatgca 60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga 120
gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc 180
ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa 240
cttccatctg ttatcactgg agaaagccca gactcccan gacnggtacg gattgtgggc 300
atanaaggat tgggtgaagc tggcgttgtg gt 332
```

&lt;210&gt; 132

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(322)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 132

```
acttttgcga ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc 60
```

```

agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat   120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt   180
tttagcaagt taaaatgaan atgacaggaa aggccttatt atcaacaaag agaagagttg   240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct   300
gtaacaatct acaattgggc ca                                     322

```

&lt;210&gt; 133

&lt;211&gt; 278

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(278)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 133

```

acaagccttc acaagtttaa cttaaattggg attaatcttt ctgtanttat ctgcataatt   60
cttggttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta   120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg   180
ctattcctgt tttgtcaaag aaatttatatt tttcaaaata tgnatatttg ttgatgggt   240
cccacgaaac actaataaaa accacagaga ccagcctg                               278

```

&lt;210&gt; 134

&lt;211&gt; 121

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(121)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 134

```

gtttanaaaa cttgtttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca   60
tgattctctg aggttaaact tggttttcaa atgttatctt tacttggtatt ttgcttttgg   120
t                                                                 121

```

&lt;210&gt; 135

&lt;211&gt; 350

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(350)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 135

```

acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc   60
atancaagtg gtgactgggt aagcgtgcga caaaggctcag ctggcacatt acttgtgtgc   120
aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca   180
gggtgcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgtc   240
ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag   300
ttcccaagga tgc aaagcct ggtgctcaac tctggggcg tcaactcagt             350

```

<210> 136  
 <211> 399  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(399)  
 <223> n = A,T,C or G

<400> 136  
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60  
 gctgtgattg tatccgaata ntcctcgtga gaaaagataa tgagatgacg tgagcagcct 120  
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180  
 cctggcggcc agccagccag ccacagggtg gcttcttctt ttgtggtga caacnccaag 240  
 aaaactgcag aggccaggg tcaggtgtna gtgggtangt gaccataaaa caccagggtgc 300  
 tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360  
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137  
 <211> 165  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(165)  
 <223> n = A,T,C or G

<400> 137  
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60  
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120  
 ttggctggtc ccactggtgg tcaactgtcat tgggtggggt cctgt 165

<210> 138  
 <211> 338  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(338)  
 <223> n = A,T,C or G

<400> 138  
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60  
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccaa 120  
 tgctgggcag tctcccatgc ctccacagt gaaagggtt gagaaaaatc acatccaatg 180  
 tcatgtgttt ccagccacac caaaagggtgc ttgggggtgga gggctggggg catananggt 240  
 cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300  
 aaaaactgat gccttttttt tttttttttt taaaattc 338

<210> 139  
 <211> 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 139

gggaatcrtg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa	60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccga gtgaaggaga	120
attcaaacag acctcgatcat tccctgggtg agcctggteg gctcaccgcc tatcatctgc	180
atttgcctta ctcaggtgct accggactct ggcccctgat gtctgtagtt tcacaggatg	240
ccttatttgt cttctacacc ccacagggcc cctacttct tcggatgtgt ttttaataat	300
gtcagctatg tgccccatcc tccttcatgc cctccctccc tttcctacca ctgctgagtg	360
gcctggaact tgtttaaagt gt	382

&lt;210&gt; 140

&lt;211&gt; 200

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (200)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 140

accaaancctt ctttctgttg tgtnngattt tactataggg gtttngcttn ttctaaanat	60
acttttcatt taacancctt tgtaagtgt caggctgcac ttgctccat anaattattg	120
ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt	180
atattcagca taaaggagaa	200

&lt;210&gt; 141

&lt;211&gt; 335

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (335)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 141

actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggtgg	60
gggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc aggggttgtt	120
atgcatgtag agaaccctaaa ctaatttatt aaacaggata gaaacaggct gtctgggtga	180
aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg	240
ttttcttacc agttcagaga tnggttaatg actanttcca atggggaaaa agcaagatgg	300
attcacaac caagtaattt taaacaaaga cactt	335

&lt;210&gt; 142

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (459)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 142

accagggttaa tattgccaca tatatccttt ccaattgcgg gctaaacaga cgtgtattta	60
gggttggtta aagacaaccc agcttaatat caagagaaat tgtgaccttt catggagtat	120
ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca	180
cacatgggtcc aacaacactc aaataataaa tcaaatatna tcagatgtta aagattgggc	240
ttcaaacatc atagccaatg atgccccgct tgcctataat ctctccgaca taaaaccaca	300
tcaacacctc agtggccacc aaaccattca gcacagcttc ctttaactgtg agctgtttga	360
agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct	420
cagcangggg gggaggaacc agctcaacct tggcgtant	459

&lt;210&gt; 143

&lt;211&gt; 140

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 143

acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg	60
aaatccaaac agtctctcct agaaaggaat agtgtcacca accccaccca tctccctgag	120
accatccgac ttcctgtgt	140

&lt;210&gt; 144

&lt;211&gt; 164

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(164)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 144

acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct	60
atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta tacaattttg	120
aggcaattaa tccatatttg ttttcaataa ggaaaaaag atgc	164

&lt;210&gt; 145

&lt;211&gt; 303

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(303)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 145

acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa	60
actggagggt atttataccc aattatecca ttcattaaca tgccctcctc ctcaggctat	120
gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgt ataaacttca	180
gtaggggagt ccatccaagt gacaggctca atcaaaggag gaaatggaac ataagcccag	240
tagtaaaaatn ttgcttagct gaaacagcca caaaagactt accgccgtgg tgattacat	300
caa	303

&lt;210&gt; 146



<211> 327  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(327)  
 <223> n = A,T,C or G

<400> 146  
 actgcagctc aattagaagt ggtctctgac ttctcatcanc ttctccctgg gctccatgac 60  
 actggcctgg agtgactcat tgctctggtt gggtgagaga gctcctttgc caacaggcct 120  
 ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180  
 cctgaacagg gaggtggga ggagccagca tggaacaagc tgccactttc taaagtagcc 240  
 agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300  
 taggggtgag ctgtgtgact ctatggt 327

<210> 147  
 <211> 173  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(173)  
 <223> n = A,T,C or G

<400> 147  
 acattgtttt tttagataa agcattgana gagctctcct taacgtgaca caatggaagg 60  
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148  
 <211> 477  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(477)  
 <223> n = A,T,C or G

<400> 148  
 acaaccactt tatctcatcg aatttttaac ccaaactcac tcaactgtgcc ttctatcct 60  
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120  
 gccctactac ctgctgcaat aatcacattc ccttctgtgc ctgacctga agccattggg 180  
 gtggctctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgtcac 240  
 nccanccac ctcaccgacc ccatectctt acacagctac ctcttgctc tctaacccca 300  
 tagattatnt ccaaattcag tcaattaagt tactattaac actctaccg acatgtccag 360  
 caccactggt aagccttctc cagccaacac acacacacac acacncacac acacacatat 420  
 ccaggcacag gctacctcat cttcacaatc acccctttaa ttaccatgct atggtgg 477

<210> 149  
 <211> 207  
 <212> DNA

<213> Homo sapien

<400> 149

acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac	60
taacgtatatt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct	120
gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca	180
tttcaggcag agggaacagc agtgaaa	207

<210> 150

<211> 111

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(111)

<223> n = A,T,C or G

<400> 150

accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg	60
cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t	111

<210> 151

<211> 196

<212> DNA

<213> Homo sapien

<400> 151

agcgcggcag gtcatatga acattccaga tacctatcat tactcgatgc tgttgataac	60
agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat	120
ggataccaac cggaaaaccc ctatcccga cagccactg tggccccac tgtctacgag	180
gtgcatccgg ctacgt	196

<210> 152

<211> 132

<212> DNA

<213> Homo sapien

<400> 152

acagcacttt cacatgtaag aaggagaaaa ttccctaaatg taggagaaaag ataacagaac	60
cttccccctt tcatctagtg gtggaaacct gatgctttat gttgacagga atagaaccag	120
gagggagttt gt	132

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(285)

<223> n = A,T,C or G

<400> 153

acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag	60
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```

cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga    120
gcacatcaat aaagtccaaa gtcttggaact tggccttggc ttggaggaag tcatcaacac    180
cctggctagt gaggggtgcg cgccgtcctt ggatgacggc atctgtgaag tcgtgcacca    240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt                      285

```

```

<210> 154
<211> 333
<212> DNA
<213> Homo sapien

```

```

<400> 154
accacagtc tgttgggcca gggcttcatt accctttctg tgaaaagcca tattatcacc    60
accccaaat tttccttaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac    120
cctaagccg ttacacagct aactcccact ggccctgatt tgtgaaattg ctgctgcctg    180
attggcacag gagtccaagg tgttcagctc cctcctccg tggaacgaga ctctgatttg    240
agtttcacaa attctcgggc cactcgtca ttgctcctct gaaataaaat ccggagaatg    300
gtcaggcctg tctcatccat atggatcttc cgg                      333

```

```

<210> 155
<211> 308
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G

```

```

<400> 155
actggaaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg    60
gaaagtgcct tgggaactgt aaagtgccta acacatgac gatgattttt gttataatat    120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc    180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggt    240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtga aggcagctg    300
gccctggt                      308

```

```

<210> 156
<211> 295
<212> DNA
<213> Homo sapien

```

```

<400> 156
accttgctcg gtgcttggaa catattagga actcaaaata tgagatgata acagtgccta    60
ttattgatta ctgagagaac tgtagacat ttagttgaag attttctaca caggaactga    120
gaataggaga ttatgtttgg cctcatatt ctctcctatc ctccttgctt cattctatgt    180
ctaatatatt ctcaatcaaa taaggtttagc ataatcagga aatcgaccaa ataccaatat    240
aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat      295

```

```

<210> 157
<211> 126
<212> DNA
<213> Homo sapien

```

```

<400> 157
acaagtttaa atagtgcgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct    60

```

gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120  
cttagt 126

<210> 158  
<211> 442  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(442)  
<223> n = A,T,C or G

<400> 158  
accactggt ctgggaaaca cccatcctta atacgatgat tttctgtcg tgtgaaaatg 60  
aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt 120  
gcctgggtaa ttcaccatta atttcctccc ccaaactctc tgagtcttcc cttaatatct 180  
ctggtgggtc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta 240  
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtg gagagtggg 300  
ccaaccctgt tttccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga 360  
nacagacggg ctctttgcag agccgggact ctgagangga catgaggggc tctgcctctg 420  
tggtcattct ctgagtccct gt 442

<210> 159  
<211> 498  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(498)  
<223> n = A,T,C or G

<400> 159  
acttccaggt aacgttggtt tttccgttga gcctgaactg atgggtgacg ttgtagggtc 60  
tccaacaaga actgagggtt cagagcgggt aggggaagagt gctgttccag ttgcacctgg 120  
gctgctgtgg actgttggtt attcctcact acggcccaag gttgtggaac tggcanaaag 180  
gtgtgttggt gganttgagc tcgggcggtt gtggtaggtt gtgggctctt caacaggggc 240  
tgctgtgggt ccggggangtg aangtggtgt gtcacttgag cttggccagc tctggaaagt 300  
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa 360  
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgten 420  
tcaggtaana atgtgggttc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc 480  
aagggataaa gctgtggt 498

<210> 160  
<211> 380  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(380)  
<223> n = A,T,C or G

<400> 160

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac 60  
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct 120  
ggagcatggc atagaggaag ctganaaatg tgggggtctga ggaagccatt tgagtctggc 180  
cactagacat ctcatcagcc acttgtgtga agagatgccc catgacccca gatgcctctc 240  
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg 300  
gagaaaaatg gcagtttgac cgaacctgtt cacaacggtg gaggtcgatt tctaacgaaa 360  
ctgtagaat gaagcctgga 390

<210> 161  
<211> 114  
<212> DNA  
<213> Homo sapien

<400> 161  
actccacatc ccctctgagc aggcggttgt cgttcaaggc gtatttgccc ttgcctgtca 60  
cactgtccac tggcccctta tccacttggt gcttaatccc tcgaaagagc atgt 114

<210> 162  
<211> 177  
<212> DNA  
<213> Homo sapien

<400> 162  
actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa 60  
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt 120  
tgggtgatata taacttggca ataaccagc ctggtgatac ataaaactac tcactgt 177

<210> 163  
<211> 137  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(137)  
<223> n = A,T,C or G

<400> 163  
catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac 60  
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt 120  
catcagcggc atgatgt 137

<210> 164  
<211> 469  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(469)  
<223> n = A,T,C or G

<400> 164  
cttatcacia tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta 60  
tgcaatgcat catgctatct catacctaag gagggagtgc caggagattc aaccaggaaa 120

```

tgcattggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt      180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg      240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg      300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct      360
tctagtaggc acagggtccc caggccaggc ctcattctcc tctggcctct aatagtcaat      420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt      469

```

&lt;210&gt; 165

&lt;211&gt; 195

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (195)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 165

```

acagtttttt atanatatcg acattgccgg cacttggtgt cagtttcata aagctgggtg      60
atccgctgtc atccactatt ccttggttag agtaaaaatt attcttatag cccatgtccc      120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact      180
tcctctgaga tgagt                                     195

```

&lt;210&gt; 166

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (383)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 166

```

acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc      60
cgaggctcga gtccacacca ccggtgtagg tgtgctcaat cttgggcttg gcgcccacct      120
ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt      180
tttgagagcc agcctgagca aggggcggat gttcagcttc agtcctcctc tcgtcagggtg      240
gatgccaacc tcgtctangg tccgtgggaa gctggtgtcc acntcaccta caacctgggc      300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt      360
nggggccttt ttggtgaact ttc                                     383

```

&lt;210&gt; 167

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (247)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 167

```

acagagccag accttggcca taaatgaanc agagattaag actaaacccc aagtcganat      60
tggagcagaa actggagcaa gaagtgggccc tggggctgaa gtagagacca aggccactgc      120

```

tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac	180
tcaatctgan tccaaagtgg tggctggaac actggctcatg acanaggcag tgactctgac	240
tgangtc	247

&lt;210&gt; 168

&lt;211&gt; 273

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(273)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 168

acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa	60
aatccctcan ccttggtctt cacnactgtc tatactgana gtgtcatgtt tccacaaagg	120
gctgacacct gagcctgnat tttactcat ccctgagaag ccctttccag taggggtggc	180
aattcccaac ttccttgcca caagcttccc aggctttctc ccctggaaaa ctccagcttg	240
agtcccagat acactcatgg gctgccttg gca	273

&lt;210&gt; 169

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(431)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 169

acagccttgg cttcccaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc	60
agctcagacc agggtc aaag gatgtgacat caacagtttc tggtttcaga acaggttcta	120
ctactgtcaa atgaccccc atacttctc aaaggctgtg gtaagttttg cacagggtgag	180
ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac	240
cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctgg gcaccagctc	300
acgcacatca ctgacaaccg ggatggaaaa agaantgcc aactttcatac atccaactgg	360
aaagtgatct gatactggat tcttaattac cttcaaaagc ttctgggggc catcagctgc	420
tcgaacactg a	431

&lt;210&gt; 170

&lt;211&gt; 266

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(266)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 170

acctgtgggc tgggctgtta tgccctgtgcc ggctgctgaa agggagttca gaggtggagc	60
tcaaggagct ctgcaggcat ttgccaanc ctctccanag canagggagc aacctacact	120
ccccgctaga aagacaccag attggagtcc tgggaggggg agttgggggtg ggcatttgat	180

gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240  
tcaaagctag gggctctggca ggtgga 266

<210> 171  
<211> 1248  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(1248)  
<223> n = A,T,C or G

<400> 171  
ggcagccaaa tcataaacgg cgaggactgc agcccgcact cgcagccctg gcaggcggca 60  
ctgggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcatecgca gtgggtgctg 120  
tcagccgcac actgtttcca gaagtgagtg cagagctcct acaccatcgg gctgggcctg 180  
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240  
cggcacccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac 300  
gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360  
gcggggaaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420  
gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac 480  
ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc 540  
aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtctttc 600  
ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtct acaccaacct ctgcaaattc 660  
actgagtggg tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720  
attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agcccctcct 780  
ccctcaggcc caggagtcca ggcgccagc ccctcctccc tcaaaccaag ggtacagatc 840  
cccagcccct cctccctcag acccaggagt ccagaccccc cagcccctcc tccctcagac 900  
ccaggagtcc agcccctcct ccctcagacc caggagtcca gacccccag cccctcctcc 960  
ctcagaccga ggggtccagg cccccaaccc ctctcctcct agactcagag gtccaagccc 1020  
ccaaccntc attcccaga cccagaggtc cagggtcccag cccctcntcc ctcagaccga 1080  
gcggtccaat gccacctaga ctntccctgt acacagtgcc cccttggtggc acgttgacct 1140  
aaccttacca gttgggtttt catTTTTngt cccttcccc tagatccaga aataaagttt 1200  
aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1248

<210> 172  
<211> 159  
<212> PRT  
<213> Homo sapien

<220>  
<221> VARIANT  
<222> (1)...(159)  
<223> Xaa = Any Amino Acid

<400> 172  
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro  
1 5 10 15  
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
20 25 30  
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
35 40 45  
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly  
50 55 60



Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu  
 65 70 75 80  
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe  
 85 90 95  
 Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser  
 100 105 110  
 Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe  
 115 120 125  
 Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn  
 130 135 140  
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 145 150 155

&lt;210&gt; 173

&lt;211&gt; 1265

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1265)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 173

```

ggcagcccg c actcgagcc ctggcaggcg gcactgggtc tggaaaacga attgttctgc      60
tcgggcgctc tgggtgatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc      120
tacaccatcg ggctgggccc gcacagtctt gaggccgacc aagagccagg gagccagatg      180
gtggaggcca gcctctccgt acggcaccca gactacaaca gaccttgct cgtctaacgac      240
ctcatgtctc tcaagttgga cgaatccgtg tccgagtctg acaccatccg gagcatcagc      300
attgttctgc agtgccctac cgcggggaac tcttgctctg cttctggctg gggctctgctg      360
gcgaacgggt agtccacggg tgtgtgtctg cctcttcaa ggaggctctc tgcccagtcg      420
cgggggctga cccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga      480
acgtgtcggt ggtgtctgag gaggtctgca gtaagctcta tgaccgctg taccacccca      540
gcatgttctg cgcggcgcca gggcaagacc agaaggactc ctgcaacggt gactctgggg      600
ggcccctgat ctgcaacggg tacttgaggg gccttgtgtc ttctggaaaa gcccgtgtg      660
gccaaagtgg cgtgccaggt gtctacacca acctctgcaa attcactgag tggatagaga      720
aaaccgtcca ggccagttaa ctctggggac tgggaaccca tgaaattgac ccccaaatac      780
atcctgcgga aggaattcag gaatatctgt tcccagcccc tctcctctca ggcccaggag      840
tccagggccc cagccccctc tccctcaaac caagggtaca gatccccagc cctcctctcc      900
tcagacccag gagtccagac cccccagccc ctctctctc agacccagga gtccagcccc      960
tctcctntca gacccaggag tccagacccc ccagcccctc ctccctcaga cccaggggtt     1020
gaggccccca accctctctc ctccagagtc agagggtcaa gcccccaacc cctcgttccc     1080
cagacccaga ggttnnaggtc ccagcccctc tctcctcaga cccagnngtc caatgccacc     1140
tagattttcc ctgnacacag tgcccccttg tggngangttg acccaacctt accagttggt     1200
ttttcatttt tngtcccttt cccttagatc cagaaataaa gtttaagaga ngngcaaaaa     1260
aaaaa                                           1265
  
```

&lt;210&gt; 174

&lt;211&gt; 1459

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1459)

<223> n = A,T,C or G

<400> 174

```

ggtcagccgc acactgtttc cagaagtgag tgcagagctc ctacaccatc gggctggggc      60
tgcacagtct tgaggccgac caagagccag ggagccagat ggtggaggcc agcctctccg      120
tacggcacc cagagtacaac agacccttgc tcgctaacga cctcatgctc atcaagtgg      180
acgaatccgt gtccgagctc gacaccatcc ggagcatcag cattgcttcg cagtgcctta      240
ccgcggggaa ctcttgcttc gtttctggct ggggtctgct ggcgaacggt gagctcacgg      300
gtgtgtgtct gccctcttca aggaggtcct ctgcccagtc gcgggggctg acccagagct      360
ctgctccca ggcagaatgc ctaccgtgct gcagtgcgtg aacgtgtcgg tgggtgtctga      420
ngaggtctgc antaagctct atgaccgct gtaccacccc ancatgttct gcgcggcg      480
agggcaagac cagaaggact cctgcaacgt gagagagggg aaaggggagg gcaggcgact      540
caggggaagg tggagaaggg ggagacagag acacacaggg ccgcatggcg agatgcagag      600
atggagagac acacaggagg acagtgacaa ctagagagag aaactgagag aaacagagaa      660
ataaacacag gaataaagag aagcaaagga agagagaaac agaaacagac atggggaggc      720
agaaacacac acacatagaa atgcagttga ccttccaaca gcatggggcc tgagggcggg      780
gacctccacc caatagaaaa tcctcttata acttttgact ccccaaaaaa ctgactagaa      840
atagcctact gttgacgggg agccttacca ataacataaa tagtcgattt atgcatacgt      900
tttatgcatt catgatatac ctttgttgga attttttgat atttctaaag tacacagtct      960
gtctgtgaat ttttttaaat tgttgcaact ctcttaaaat ttttctgatg tgtttattga     1020
aaaaatccaa gtataagtgg acttgtgcat tcaaaccagg gttgttcaag ggtcaactgt     1080
gtacccagag ggaacacgtg acacagattc atagaggtga aacacgaaga gaaacaggaa     1140
aatcaagac ttacaaaga ggtgggcag ggtggctcat gcctgtaac ccagcacttt     1200
gggaggcgag gcaggcagat cacttgagggt aaggagtcca agaccagcct ggccaaaatg     1260
gtgaaatcct gtctgtacta aaaatacaaa agttagctgg atatggtggc aggcgcctgt     1320
aatccagct acttggagg ctgaggcagg agaattgctt gaatatggga ggcagaggtt     1380
gaagtgaagt gagatcacac cactatactc cagctggggc aacagagtaa gactctgtct     1440
caaaaaaaaa aaaaaaaaaa                                     1459

```

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (1167)

<223> n = A,T,C or G

<400> 175

```

gcgcagccct ggcaggcggc actggtcagt gaaaacgaat tgttctgctc gggcgctcctg      60
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg      120
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc      180
ctctccgtac ggcacccaga gtacaacaga ctcttgctcg ctaacgacct catgctcatc      240
aagtggacg aatccgtgtc caggtctgac accatccgga gcatcagcat tgcttcgag      300
tgccctaccg cggggaactc ttgcctcgtn tctggtggg gtctgctggc gaacggcaga      360
atgcctaccg tgctgcaact cgtgaacgtg tcgggtggtg ctgaggangt ctgcagtaag      420
ctctatgacc cgctgtacca cccagcagt ttctgcgccg gcggagggca agaccagaag      480
gactcctgca acggtgactc tggggggccc ctgatctgca acgggtactt gcagggcctt      540
gtgtctttcg gaaaagcccc gtgtggccaa cttggcgctg cagggtgtct caccaacctc      600
tgcaaatcca ctgagtggat agagaaaacc gtccagncca gttaactctg gggactggga      660
acccatgaaa ttgaccccca aatacatcct gcggaangaa ttcaggaata tctgttccca      720
gccctctctc cctcaggccc aggagtccag gccccagcc cctcctcctt caaaccaagg      780
gtacagatcc ccagccctc ctccctcaga cccaggagtc cagaccccc agccctctnt      840
ccttcagacc caggagtcga gccctctc cctcagacgc aggagtccag acccccagc      900

```

```

ccntcntccg tcagaccag ggggtgcaggc ccccaacccc tcntcentca gagtcagagg      960
tccaagcccc caacccctcg tccccagac ccagaggtn c aggtcccagc cctcctccc      1020
tcagaccag cgggtccaatg ccacctagan tntcctgtg cacagtgcc ccttggtggca      1080
ngttgacca accttaccag ttgggtttttc atttttgtg cctttccctt agatccagaa      1140
ataaagtnta agagaagcgc aaaaaaa      1167

```

<210> 176  
 <211> 205  
 <212> PRT  
 <213> Homo sapien

<220>  
 <221> VARIANT  
 <222> (1)...(205)  
 <223> Xaa = Any Amino Acid

<400> 176

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10					15	
Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
			20					25					30		
Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
		35					40					45			
Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Leu	Leu	Leu
	50					55					60				
Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
65					70				75					80	
Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
			85					90					95		
Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met
		100						105					110		
Pro	Thr	Val	Leu	His	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Xaa	Val
		115					120					125			
Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala
	130					135					140				
Gly	Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly
145					150				155					160	
Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys
			165					170					175		
Ala	Pro	Cys	Gly	Gln	Leu	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys
		180						185					190		
Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Xaa	Ser			
		195					200					205			

<210> 177  
 <211> 1119  
 <212> DNA  
 <213> Homo sapien

<400> 177

```

gcgcactcgc agccctggca ggcggcactg gtcattgaaa acgaattggt ctgctcgggc      60
gtccctgggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctccctacacc      120
atcgggctgg gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatgggtggag      180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300

```

```

tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctggggtct gctggcgaac 360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420
caacctgggc agggttgtac catttcggca acttccagtg caaggacgtc ctgctgcatc 480
ctcactgggt gctcactact gctcactgca tcacccggaa cactgtgac aactagccag 540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc 720
tgacctacag aggtgaggga tcatatagct ctccaaggat gctgggtactc ccctcacaaa 780
ttcatttctc ctggtttagt gaaagggtgc ccctctggag cctcccaggg tgggtgtgca 840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg 900
ctcagtacac cagggcaggt ctagcatttc ttcathtagt gtatgctgtc cattcatgca 960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg 1020
gaggtgaggg agagggccca tgggtcaatg ggatctgtgc agttgtaaca cattaggtgc 1080
ttaataaaca gaagctgtga tgtaaaaaa aaaaaaaaa 1119

```

&lt;210&gt; 178

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(164)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 178

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100          105          110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115          120          125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130          135          140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145          150          155          160
Pro Gly Thr Leu

```

&lt;210&gt; 179

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 179

```

ctggagtgcc ttggtgtttc aagccctgc aggaagcaga atgcaccttc tgaggcacct    60
ccagctgccc ccggccgggg gatgagaggc tcggagcacc cttgcccggc tgtgattgct    120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga    180
aagttcatat ctggagcctg atgtcttaac gaataaaggc cccatgctcc acccgaaaaa    240
aaaaaaaaaa                                     250

```

&lt;210&gt; 180

&lt;211&gt; 202

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 180

```

actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca    60
tcacccagac ccgcccctg cccgtgcccc acgctgctgc taacgacagt atgatgctta    120
ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttggt tataaatgcc    180
tgatttaaaa aaaaaaaaaa aa                                     202

```

&lt;210&gt; 181

&lt;211&gt; 558

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(558)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 181

```

tccytttgkt naggtttkkg agacamceek agacctwaan ctgtgtcaca gacttcyngg    60
aatgtttagg cagtgctagt aatttcytcg taatgattct gttattactt tcctnattct    120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa    180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca    240
aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac    300
ctactctgtt ccttggttag aaaaaattat aaacaggact ttgttagttt gggaagccaa    360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw    420
ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt    480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc    540
caaaaaaaaa aaaaaaaaaa                                     558

```

&lt;210&gt; 182

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(479)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 182

```

acagggwttk grggatgcta agsecccrga rwtggtttga tccaacctg gcttwttttc    60
agaggggaaa atggggccta gaagttacag mscatytagy tggtagcmgtg gcacccctgg    120
cstcacacag astcccgagt agctgggact acaggcacac agtcactgaa gcaggccctg    180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca    240
ctaagggttaa actttcccac ccagaaaagg caacttagat aaaatcttag agtactttca    300

```

tactmttcta agtctctctc cagcctcact kkgagtctcm cytggggggt gataggaant	360
ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg tacgcataa	420
awtgstgara aaattaaaat gttctggtty macttttaaaa araaaaaaaa aaaaaaaaa	479

&lt;210&gt; 183

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 183

agggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactgggtgcc	60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgc	120
gggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt	180
gccagcacca gtggcagctc tgggtgcctgt gggttctcct acaagtgaga ttttagatat	240
tgtaaatcct gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca	300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aractctatt	360
gccatttcaa aaaaaaaaaa aaaa	384

&lt;210&gt; 184

&lt;211&gt; 496

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (496)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 184

accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatcac ctcaacgagc	60
agggagatcg agtctatacg ctgaagaaat ttgacccgat gggacaacag acctgctcag	120
cccatcctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga	180
aacgcttcaa ggtgctcatg acccagcaac cgcgcctgt cctctgaggg tcccttaaac	240
tgatgtcttt tctgccacct gttacccctc ggagactccg taaccaaact cttcggactg	300
tgagccctga tgctttttt ccagccatac tctttggcat ccagtctctc gtggcgattg	360
attatgcttg tgtgaggcaa tcatgggtggc atcaccata aagggaacac atttgacttt	420
ttttctcat attttaaat actacmagaw tattwmagaw waaatgawtt gaaaaactst	480
taaaaaaaa aaaaaa	496

&lt;210&gt; 185

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 185

gctggtagcc tatggcgkgg cccacggagg ggctcctgag gccacggrac agtgacttcc	60
caagtatcyt gcgcsgcgtc ttctaccgtc cctacctgca gatcttcggg cagattcccc	120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggcttct	180
gggcacaccc tcctggggcc caggcgggca cctgcgtctc ccagtatgcc aactggctgg	240
tgggtgctgt cctcgtcctc ttctgctcgt tggccaacat cctgctggtc aacttgctca	300
ttgccatggt cagttacaca ttccggcaaag tacagggcaa cagcgatctc tactgggaag	360
gcgcagcgtt accgcctcat ccgg	384

&lt;210&gt; 186

&lt;211&gt; 577

<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(577)  
<223> n = A,T,C or G

<400> 186

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gcntaatatt	120
ccaggaaact	ctcaatcaag	tcaccgtcga	tgaaacctgt	gggctgggtc	tgtcttccgc	180
tcgggtgtgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtagcag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mcgtgccgaa	garcaccgag	ccttgtgtgg	gggkkgaaagt	360
ctcaccacaga	ttctgcatta	ccagagagcc	gtggcaaaaag	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttggt	ggcagcgctw	480
tccttttgac	acacaaaaca	gttaaaggca	tttccagccc	ccagaaantt	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

<210> 187  
<211> 534  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(534)  
<223> n = A,T,C or G

<400> 187

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctgggtattaa	aattcacaat	atgcaacact	120
ttaaacagtg	tgtaaatctg	ctcccyynac	tttgtcatca	ccagtctggg	aakaagggtta	180
tgccctatcc	acacctgtta	aaagggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatggggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttyggggagc	360
tgatatttga	gcggaagagt	agccttttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agttttattta	ccacttgcac	aagaaggcgt	tttcttcttc	agge	534

<210> 188  
<211> 761  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(761)  
<223> n = A,T,C or G

<400> 188

agaaaccagt	atctctnaaa	acaacctctc	ataccttggtg	gacctaat	ttt	60
tgtgtgtgcg	cgcataattat	atagacaggc	acatcttttt	tacttttgta	aaagcttatg	120
cctctttgggt	atctatctct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggaccc	180

```

ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg      300
ggggacaaag aaaagcaaaa ctgamcataa raaacaatwa cctgggtgaga arttgcataa      360
acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt      420
gcaaaaaaca tgtacngact tcccgttgag taatgccaaag ttgttttttt tatnataaaa      480
cttgcccttc attacatggt tnaaagtggt gtgggtgggccc aaaatattga aatgatggaa      540
ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatggtgac      600
atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta      660
tttttctgtn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac      720
gaaaataata acattgaaga aaananaaaa aaanaaaaaa a                          761

```

&lt;210&gt; 189

&lt;211&gt; 482

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(482)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 189

```

- tttttttttt tttgccgatn ctactatntt attgcaggan gtgggggtgt atgcaccgca      60
caccggggct atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca      120
aagccgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc      180
aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggangtgt gcataagaag      240
tgataggcac aggccaccgc gtacagaccc ctcggtctct gacaggtnga tttcgaccag      300
gtcattgtgc cctgccaggc cacagcgtan atctggaaaa gacagaatgc tttccctttc      360
aaatttggtc ngtcatngaa ngggcanttt tccaanttng gctnggtctt ggtacncttg      420
gttcggccca gctcncgtc caaaaantat tcaccnncct ccnaattgct tgcnggnccc      480
cc

```

&lt;210&gt; 190

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(471)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 190

```

tttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtggttttg      60
aaaactctcg catccagtga gaactaccat acaccacatt acagctngga atgtntcca      120
aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag      180
cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt      240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt      300
tgaaaaattt catgtatgca atccaaccaa agaacttnat tggatgatcat gantnctcta      360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacnngt acaaaaaanaa      420
tctgtaattn anttcaacct ccgtacngaa aaatnttntt tatacactcc c                          471

```

&lt;210&gt; 191

&lt;211&gt; 402

&lt;212&gt; DNA



<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(402)

<223> n = A,T,C or G

<400> 191

gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct	60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa	120
attcttcacc agtcacatct tctaggacct ttttggattc agttagtata agctcttcca	180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg	240
ctcgttctct aacaatgtcc tctccttgaa gtatttggtc gaacaaccca cctaaagtcc	300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggc taaattctgc	360
aagagtcac tgtctgcaaa agttgcgtta gtatatctgc ca	402

<210> 192

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(601)

<223> n = A,T,C or G

<400> 192

gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac	120
atgcytyttt gaytaccgtg tgccaagtgc tgggtgattct yaacacacyt ccatcccgyt	180
cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc	240
acgagacact tgaaagggtg aacaaagcga ytcttgcatc gctttttgtc cctccggcac	300
cagttgtcaa tactaaccgc ctggtttgcc tccatcacat ttgtgatctg tagctctgga	360
tacatctcct gacagtactg aagaacttct tcttttgttt caaaagcarg tcttggtgcc	420
tggtggatca ggttcccatt tcccagtcyg aatgttcaca tggcatattt wacttcccac	480
aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag	540
cctcgatgta gccggccagc gccaaaggcag gcgccgtgag cccaccagc agcagaagca	600
g	601

<210> 193

<211> 608

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(608)

<223> n = A,T,C or G

<400> 193

atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact	60
ggtcccgtg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcytt	120
cccaacgcag gcagmagcgg gscgggtcaa tgaactccay tcgtggcttg gggtkgacgg	180
tkaagtgcag gaagaggctg accacctcgc ggtccaccag gatgcccagc tgtgcgggac	240
ctgcagcgaa actcctcgat ggtcatgagc gggaaagcgaa tgaggcccag ggccttgccc	300

```

agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctgggcctcg   360
gaccagcggg caaacgggct tgaacagccg cacctcacgg atgcccagtg tgcgcgctc   420
caggammgsc accagcgtgt ccagggtcaat gtcgggtgaag ccctccgagg gtrattggcg   480
ctgcagtggt tttgtcgatg ttctccaggc acaggctggc cagctgcggg tcatcgaaga   540
gtcgcgcctg cgtgagcagc atgaaggcgt tgcgggctcg cagttcttct tcaggaaactc   600
cacgcaat                                     608

```

&lt;210&gt; 194

&lt;211&gt; 392

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(392)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 194

```

gaacggctgg accttgccct gcattgtgct tgctggcagg gaataccttg gcaagcagyt   60
ccagtcgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc   120
tccgcctcaa tgcagaacca gtatggggag cactgtgttt agagttaaga gtgaacactg   180
tttgatttta cttgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac   240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagtaggtg attctgtatt   300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktnctstgg   360
aaataaatat agttattaaa gggtgtcant cc                                     392

```

&lt;210&gt; 195

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(502)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 195

```

ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg   60
ccgagctgag gcagatgttc ccacagtgc cccagagacc stgggstata gtytctgacc   120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc   180
aagggaaggc cccattccgg ggstgttccc cgaggaggaa ggaaggggc tctgtgtgcc   240
ccccasgagg aagaggccct gagtccctgg atcagacacc ccttcacgtg tatccccaca   300
caaattgcaag ctaccaagg tcccctctca gtccccttcc stacacctg amcggccact   360
gscscacacc caccagagc acgccacccg ccatggggar tgtgctcaag gartcgcnng   420
gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt   480
gctnanaaaa aaaaaanaaa aa                                     502

```

&lt;210&gt; 196

&lt;211&gt; 665

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(665)

<223> n = A,T,C or G

<400> 196

```

ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc    60
cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt    120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga    180
actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkac    240
aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt    300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgaact    360
tcacttggtt attttattgt aaatgattta caaaattctt aatttaagar aatggtatgt    420
watatttatt tcattaattt ctttcctkgt ttacgtwaat ttgaaaaga wtgcatgatt    480
tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt    540
ttcttagaat gtataaagggt tgtagcccat cnaacttcaa agaaaaaat gaccacatac    600
tttgcataca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan    660
aagtg

```

<210> 197

<211> 492

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (492)

<223> n = A,T,C or G

<400> 197

```

tttntttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat    60
atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg    120
aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag    180
aattatagtc naaccagtaa acnaggaatt tactttttcaa aagattaaat ccaaactgaa    240
caaaattcta cctgaaact tactccatcc aaatattgga ataanagtca gcagtgatac    300
attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct    360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc    420
catttcactc ccatcacggg agtcaatgct acctgggaca cttgtatttt gtccatnctg    480
ancntggctt aa

```

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1) ... (478)

<223> n = A,T,C or G

<400> 198

```

tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa    60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac    120
tgagtatatt ttgaaaagga caagttttaa gtanacncat attgccganc atancacatt    180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat    240
natatatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag    300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta    360
agcattctag tacctctact ccatggttaa gaatcgtaca cttatgttta catatgtnca    420

```

gggtaagaat tgtgttaagt naanttatgg agaggtccan gagaaaaatt tgatncaa 478

<210> 199

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 199

agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta	60
tgctagttcc tgtcatctat tcgctactaa atgcagactg gaggggacca aaaaggggca	120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga	180
agtgattcag tttcctctac ggatgagaga ctgggtcaag aatatacctca tgcagcttta	240
tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga	300
aaatttacct ggangaaaag aggcttngg ctggggacca tccattgaa cttctcttta	360
anggacttta agaanaaact accacatgtn tgtngtatcc tgggtgccngg ccgtttantg	420
aacntngacn ncacccttnt ggaatanant cttgacngcn tcctgaactt gtcctctctgc	480
ga	482

<210> 200

<211> 270

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(270)

<223> n = A,T,C or G

<400> 200

cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgccca gcagttggtc	60
cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc	120
aaggctgagc tgacgccgca gaggtcgtgt cacgtccacac gaccttgacg ccgtcgggga	180
cagccggaac agagcccgtt gaangcggga ggcctcgggg agcccctcgg gaagggcggc	240
ccgagagata cgcaggtgca ggtggccgcc	270

<210> 201

<211> 419

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(419)

<223> n = A,T,C or G

<400> 201

tttttttttt ttttggaaac tactgagagc acagcaggtc agcaacaagt ttattttgca	60
gctagcaagg taacagggga gggcatggtt acatgttcag gtcaacttcc ttgtcgtgg	120
ttgattcgtt tgtctttatg ggggcggggg ggggtagggg aaancgaagc anaantaaca	180
tggagtgggt gcacctccc tgtagaacct ggttacnaaa gcttggggca gtccacctgg	240

tctgtgaccg	tcattttctt	gacatcaatg	ttattagaag	tcaggatata	ttttagagag	300
tccactgtnt	ctggagggag	attaggggtt	cttgccaana	tccaancaa	atccacntga	360
aaaagttgga	tgatncangt	acngaatacc	ganggcatan	ttctcatant	cggtggcca	419

&lt;210&gt; 202

&lt;211&gt; 509

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(509)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 202

tttntttttt	ttttttttt	ttttttttt	ttttttttt	ttttttttt	ttttttttt	60
tggcacttaa	tccattttta	tttcaaaatg	tctacaaant	ttnaatncnc	cattatacng	120
gtnattttnc	aaaatctaaa	nnttattcaa	atnfnagcca	aantccttac	ncaaatnnaa	180
tacnncaaa	aatcaaaaaa	atacntntct	ttcagcaaac	ttngttacat	aaattaaaaa	240
aatatatacg	gctgggtgtt	tcaaagtaca	attatcttaa	cactgcaaac	atnttttnaa	300
ggaactaaaa	taaaaaaaaa	cactnccgca	aagggttaaag	ggaacaacaa	attcntttta	360
caacancnnc	nattataaaa	atcatatctc	aaatcttagg	ggaatatata	cttcacacng	420
ggatcttaac	ttttactnca	ctttgtttat	ttttttanaa	ccattgtntt	gggcccaca	480
caatggnaat	nccnccnnc	tggaactagt				509

&lt;210&gt; 203

&lt;211&gt; 583

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(583)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 203

ttttttttt	tttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaatggaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tccctattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaca	ggaagagana	atggcacaca	aaacaaacat	tttatattca	tattttctacc	420
tacgttaata	aaatagcatt	ttgtgaagcc	agctcaaaag	aaggccttaga	tccttttatg	480
tccatttttag	tcactaaacg	atatcnaaag	tgccagaatg	caaaagggtt	gtgaacattt	540
attcaaaagc	taatataaga	tatttcacat	actcatcttt	ctg		583

&lt;210&gt; 204

&lt;211&gt; 589

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(589)

<223> n = A,T,C or G

<400> 204

ttttttttnt tttttttttt ttttttntct tttttttttt ttganaatga ggatcgagtt	60
tttactctc tagatagggc atgaagaaaa ctcactcttc cagctttaaa ataacaatca	120
aactctttat gctatatcat attttaagtt aaactaatga gtcactggct tatcttctcc	180
tgaaggaaat ctgttcattc ttctcattca tatagtata tcaagtacta ccttgcatat	240
tgagagggtt ttcttctcta ttacacata tatttccatg tgaatttgta tcaaaccctt	300
attttcatgc aaactagaaa ataatgtntt cttttgcata agagaagaga acaatatnag	360
cattacaaaa ctgctcaaat tgtttgttaa gnttatccat tataattagt tnggcaggag	420
ctaatacaaa tcacatttac ngacnagcaa taataaaact gaagtaccag ttaaatatcc	480
aaaataatta aaggacatt tttagcctgg gtataattag ctaattcact ttacaagcat	540
ttattnagaa tgaattcaca tgttattatt centagccca acacaatgg	589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

ttttntttt ttttttcagt aataatcaga acaatattta tttttatatt taaaattcat	60
agaaaagtgc cttacattta ataaaagttt gtttctcaaa gtgatcagag gaattagata	120
tngtcttgaa caccaatatt aatttgagga aaatacacca aaatacatta agtaaattat	180
ttaagatcat agagcttgta agtgaaaaga taaaatttga cctcagaaac tctgagcatt	240
aaaaatccac tattagcaaa taaattacta tggacttctt gctttaattt tgtgatgaat	300
atgggggtgc actggtaaac caacacattc tgaaggatac attacttagt gatagattct	360
tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt	420
aaggggcnga ngaatgagg aagaaaagaa aaggattacg catactgttc ttctatnngg	480
aaggattaga tatgtttcct ttgccaatat taaaaaata ataatgttta ctactagtga	540
aaccc	545

<210> 206

<211> 487

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

ttttttttt ttttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt	60
catttattag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna	120
caatttataa atgtaagggtg ccattattga gtanatatat tctccaaga gtggatgtgt	180
cccttctccc accaactaat gaancagcaa cattagttaa attttattag tagatnatac	240
actgctgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag	300
ttggtnagaa tgcatcanca atctnacaat caacagcaag atgaagctag gcntgggctt	360
tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cgggtggcaag	420
aactcttcga accgcttctt caaaggcngc tgccacattt gtggcntctn ttgcacttgt	480

ttcaaaa

487

&lt;210&gt; 207

&lt;211&gt; 332

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(332)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 207

tgaattggct	aaaagactgc	atTTTTanaa	ctagcaactc	ttatttcttt	cctttaaaaa	60
tacatagcat	taaateccaa	atcctattta	aagacctgac	agcttgagaa	ggtcactact	120
gcatttatag	gaccttctgg	tggttctgct	gttacntttg	aantctgaca	atccttgana	180
atctttgcat	gcagaggagg	taaaaggat	tggattttca	cagaggaana	acacagcgca	240
gaaatgaagg	ggccaggctt	actgagcttg	tccactggag	ggctcatggg	tgggacatgg	300
aaaagaaggc	agcctaggcc	ctggggagcc	ca			332

&lt;210&gt; 208

&lt;211&gt; 524

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(524)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 208

agggcggtgt	gcggaggggc	ttactgtttt	gtctcagtaa	caataaatac	aaaaagactg	60
gttggtgttc	ggcccatcc	aaccacgaag	ttgatttctc	ttgtgtgcag	agtgactgat	120
tttaaaggac	atggagcttg	tcacaatgtc	acaatgtcac	agtgtgaagg	gcacactcac	180
tcccgcgtga	ttcacattta	gcaaccaaca	atagctcatg	agtccatact	tgtaaatact	240
tttggcagaa	tacttnttga	aacttgcaga	tgataactaa	gatccaagat	atttcccaaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgtcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

&lt;210&gt; 209

&lt;211&gt; 159

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 209

gggtgaggaa	atccagagtt	gccatggaga	aaattccagt	gtcagcattc	ttgtctcttg	60
tggccctctc	ctacactctg	gccagagata	ccacagtcaa	acctggagcc	aaaaaggaca	120
caaaggactc	tcgacccaaa	ctgccccaga	ccctctcca			159

&lt;210&gt; 210

&lt;211&gt; 256

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(256)  
 <223> n = A,T,C or G

<400> 210  
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 actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120  
 tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180  
 ttgcaggggtg naaatgggan ggctgggttg ttanatgaac agggacatag gaggtaggca 240  
 ccaggatgct aaatca 256

<210> 211  
 <211> 264  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(264)  
 <223> n = A,T,C or G

<400> 211  
 acattgtttt tttagataa agcattgaga gagctctcct taacgtgaca caatggaagg 60  
 actggaacac ataccacat cttgttctg agggataatt ttctgataaa gtcttgctgt 120  
 atattcaagc acatatgtta tatattatc agttccatgt ttatagccta gttaaggaga 180  
 ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga 240  
 aaaaaaggag caaatgagaa gcct 264

<210> 212  
 <211> 328  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(328)  
 <223> n = A,T,C or G

<400> 212  
 acccaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa 60  
 ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120  
 gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180  
 ttnaatttca tttccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta 240  
 cccctachac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca 300  
 ttttttttct cttttattcct ttgtcaga 328

<210> 213  
 <211> 250  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature



&lt;222&gt; (1) ... (250)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 213

acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt	60
taaagcattg ctccactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgcca aagganatat acattttcaat tctccaaact tcttctctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatata tctctnacct	240
tctcatcggt	250

&lt;210&gt; 214

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (444)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 214

acccagaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag	60
gatttaattg tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg	120
tttatatag cagcaacaat attcaagcgc gacaacaggt tattgaactt gcccgccagt	180
tgaatttcac tcccattgac ttgggaccc tatcatcagc canagagatt gaaaatttac	240
ccctacgact ctttactctc tggagagggc cagtgggtgt agctataagc ttggccacat	300
ttttttttcc tttattcctt tgtcagagat gcgattcacc catatgctan aaaccaacag	360
agtgactttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt	420
actttgctct ccctaataata cctc	444

&lt;210&gt; 215

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (366)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 215

acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt	60
taaagcattg ctccactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgcca aagganatat acattttcaat tctccaaact tcttctctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct	240
tctcatcggt aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa	300
tccaagctgt tttctacact gtaaccaggt ttccaaccaa ggtggaaatc tcttatactt	360
ggtgcc	366

&lt;210&gt; 216

&lt;211&gt; 260

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

<221> misc\_feature  
 <222> (1)...(260)  
 <223> n = A,T,C or G

<400> 216  
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60  
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnctnc atttttttat 120  
 taataaaaag trnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa 180  
 atcaaaaatt tectnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240  
 aattcttctt tccctccttt 260

<210> 217  
 <211> 262  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(262)  
 <223> n = A,T,C or G

<400> 217  
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60  
 tcttgcttat aattttctat tttataagg aaatagcaaa ttgggggtggg gggaatgtag 120  
 ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180  
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240  
 atatccttca tgcttgtaaa gt 262

<210> 218  
 <211> 205  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(205)  
 <223> n = A,T,C or G

<400> 218  
 accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60  
 cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120  
 aggcctcccc agttctactg acctttgtcc ttangtntha ngtccagggt tgctaggaaa 180  
 anaaatcagc agacacaggt gtaaa 205

<210> 219  
 <211> 114  
 <212> DNA  
 <213> Homo sapien

<400> 219  
 tactgttttg tctcagtaac aataaataca aaaagactgg ttgtgttccg gccccatcca 60  
 accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220  
 <211> 93

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 220

actagccagc acaaaaaggca gggtagcctg aattgctttc tgctccttac atttctttta	60
aaataagcat ttagtgctca gtcctactg agt	93

&lt;210&gt; 221

&lt;211&gt; 167

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (167)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 221

actangtgca ggtgcgcaca aatatttgtc gatattccct tcctcttgga ttccatgagg	60
tcctttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc	120
ccccactac cttccctgac gctcccccana aatcacccaa cctctgt	167

&lt;210&gt; 222

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 222

agggcgtggg gcggaggggc gtactgacct cattagtagg aggatgcatt ctggcacccc	60
gttcttcacc tgcCCCCaa tccttaaaag gccatactgc ataaagtcaa caacagataa	120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa	180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt	240
taggtgagca tgattagaga gcttgtaggt tgcttttaca tatatctggc atatttgagt	300
ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t	351

&lt;210&gt; 223

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (383)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 223

aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat	60
tggttaattat ggtcaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga	120
ttaaaatgtc tgtgccaaaa ttttgtattt tatttgagga cttcttatca aaagtaatgc	180
tgccaaagga agtctaagga attagtagtg ttcccmccac ttgtttggag tgtgctattc	240
taaaagattt tgatttcctg gaatgacaat tatattttta ctttggtggg ggaaanagtt	300
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg	360
accattaagc tatatgttta aaa	383

&lt;210&gt; 224

<211> 320  
 <212> DNA  
 <213> Homo sapien

<400> 224  
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 aaaagtttgt gacattgtag tagggagtgt gtacccctta cccccatca aaaaaaaaaat 120  
 ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa 180  
 gagaaaatac tactttctcr aaatggaagc ccttaaaggt gctttgatac tgaaggacac 240  
 aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgcaagt 300  
 tttaractcm gcattgtgac 320

<210> 225  
 <211> 1214  
 <212> DNA  
 <213> Homo sapien

<400> 225  
 gaggactgca gccgcactc gcagccctgg caggcggcac tgggtcatgga aaacgaattg 60  
 ttctgctcgg gcgtcctggt gcaccccgag tgggtgctgt cagccgcaca ctgtttccag 120  
 aactcctaca ccacgaggct gggcctgcac agtcttgagg ccgaccaaga gccagggagc 180  
 cagatggtgg aggccagcct ctccgtacgg caccagagt acaacagacc cttgctcgct 240  
 aacgacctca tgcctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300  
 atcagcattg cttcgcagtg ccctaccgcg gggaaactctt gcctcgtttc tggctgggt 360  
 ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 420  
 gaggaggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatgtt ctgcgccggc 480  
 ggagggcaag accagaagga ctccctgcaac ggtgactctg gggggccctt gatctgcaac 540  
 gggtaacttg agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca 600  
 ggtgtctaca ccaacctctg caaatcact gagggtatag agaaaaccgt ccaggccagt 660  
 taactctggg gactgggaac ccataaaatt gacccccaaa tacatcctgc ggaaggaatt 720  
 caggaatata tgttccagc ccctcctccc tcaggccagc gaggccagcc cccagacccc 780  
 tcctccctca aaccaagggt acagatcccc agccctcctt ccctcagacc caggagtcca 840  
 gacccccag ccctcctcc ctccagacca ggagtccagc ccctcctccc tcagacccag 900  
 gaggccagac cccccagccc ctccctccctc agaccaggg gtccaggccc ccaacccctc 960  
 ctccctcaga ctccagaggtc caagccccc acccctcctt cccagacccc agagggtccag 1020  
 gtccccagccc ctccctccctc agaccagcg gtccaatgcc acctagactc tcctgttaca 1080  
 cagtgcctcc ttgtggcacg ttgacccaac cttaccagtt ggtttttcat tttttgtccc 1140  
 tttcccttag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaaaaaaaa aaaa 1214

<210> 226  
 <211> 119  
 <212> DNA  
 <213> Homo sapien

<400> 226  
 acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa 60  
 agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<400> 227

acaattcata	gggacgacca	atgaggacag	ggaatgaacc	cggtctcccc	ccagccctga	60
tttttgctac	atatggggtc	ccttttcatt	ctttgcaaaa	acactgggtt	ttctgagaac	120
acggacgggt	cttagcacia	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
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gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgctcccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttcct	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaaggggtg	caccctcagc	agagaagccg	agagcttaac	tctggctcgt	tccagagaca	480
acctgctggc	tgtcttgga	tgcgcccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcagagagg	600
gacaggctct	gccctcaagc	cggtcgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggt	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtctgtg			818

&lt;210&gt; 228

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 228

actggagaca	ctggtgaact	tgatcaagac	ccagaccacc	ccaggctctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaaacga	gcctcctcct	tggaagatgg	aagaccgtgt	120
tcgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcggagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcactgt	ggaactacca	aatggcgaga	240
tgctcgggtgc	acattgggggt	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtc	acctctgcag	360
gctggcagct	gaatggcttg	ccggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccaggttgg	480
ccagacgggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctgggtga	cagtgaacccg	540
ccgtgggtatg	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttgggggtttg	600
ttcttttcgt	taatgttcct	ctgtgtgtgc	agctgtcttc	atttcctggg	ctaagcagca	660
ttgggagatg	tggaccagag	atccactcct	taagaaccag	tggcgaaaga	cactttcttt	720
cttccactctg	aagtagctgg	tggt				744

&lt;210&gt; 229

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcagtgaac	60
cattacacat	cgaaataaaa	gaaaggtggc	agacttgccc	aacgccaggc	tgacatgtgc	120
tgcaggggtg	ttgtttttta	attattattg	ttagaaacgt	caccacaggt	ccctgttaat	180
ttgtatgtga	cagccaactc	tgagaaggtc	ctatttttcc	acctgcagag	gatccagttc	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

&lt;210&gt; 230

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 230

cagcagaaca	aatacaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120

caatataaag tcctggttca cactcaggaa cgagagctga cccagttaag ggagaagttg 180  
 cgggaaggga gagatgcctc cctctcattg aatgagcatc tccaggccct cctcactccg 240  
 gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac 300  
 g 301

<210> 231  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 231  
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 caggaactcc aagtccacat ccttggcaac tggggacttg cgcagggttag ccttgaggat 120  
 ggcaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180  
 tctgaggatg gcaggatcaa tgatgtcagg ccggttggtt ccgccaatga tgaacacatt 240  
 tttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc 300  
 c 301

<210> 232  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 232  
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 ggcgacagcg gggcttcctg attctggaat ataactttgt gttaaattaac agccacctat 120  
 agaagagtcc atctgctgtg aaggagagac agagaactct ggggtccgtc gtccctgtcca 180  
 cgtgctgtac caagtgtcgg tgccagcctg ttacctgttc tccactgaaa tctggctaata 240  
 gctcttctgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact 300  
 g 301

<210> 233  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 233  
 atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag 60  
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 cctagaagtt acagagcatc tagctgggtc gctggcaccc ctggcctcac acagactccc 180  
 gagtagctgg gactacaggc acacagtcac tgaagcaggc cctggttagca attctatgcg 240  
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 c 301

<210> 234  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 234  
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 cattttattc atcatgatgc ttctttttgt ttcttctttt cgttttcttc tttttctttt 120  
 tcaatttcag caacatactt ctcaaattct tcaggattta aaatcttgag ggattgatct 180  
 cgctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc 240  
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t		301
<210> 235		
<211> 283		
<212> DNA		
<213> Homo sapien		
<400> 235		
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tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata	180	
atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatcaaca	240	
ttagggattc aaagaaatat tagatttaag ctcacactgg tca	283	
<210> 236		
<211> 301		
<212> DNA		
<213> Homo sapien		
<400> 236		
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aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg	120	
tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatag	180	
tgggtagacg gcttcatgag tacagtgtac tgtggatcg taatctggac ttgggttgta	240	
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a	301	
<210> 237		
<211> 301		
<212> DNA		
<213> Homo sapien		
<400> 237		
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actcaatttt tgttcgctcc tttttggcct ttccaattt gtccatctca attttctggg	120	
ccttggctaa tgcctcatag taggagtcct cagaccagcc atggggatca aacatatact	180	
ttgggtagtt ggtgccaaagc tgcgtaatgg cacagaatgg atcagcttct cgtaaatcta	240	
gggttccgaa attctttctt cctttggata atgtagttca tatccattcc ctcttttatt	300	
t	301	
<210> 238		
<211> 301		
<212> DNA		
<213> Homo sapien		
<400> 238		
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ccttgagact tccggagtcg aggtcttcca gggttcccca gcccatcaat cattttctgc	180	
acccccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca	240	
gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttcttta	300	
t	301	
<210> 239		
<211> 239		

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 239

ataagcagct aggggaattct ttatttagta atgtcctaac ataaaagtgc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgccca gcatacacag tatacaggtc cttcaggga	239

&lt;210&gt; 240

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 240

ggtcctaagt aagcagcagc ttccacattt taacgcaggt ttacggtgat actgtccttc	60
gggatctgcc ctccagtgga accttttaag gaagaagtgg gcccaagcta agttccacat	120
gctgggtgag ccagatgact tctgttcctt ggctactttc ttcaatgggg cgaatggggg	180
ctgccagggt tttaaaatca tgcttcattt tgaagcacac ggctacttca ccttcctcac	240
gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc	300

&lt;210&gt; 241

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 241

gaggctctggt gctgaggtct ctgggctagg aagaggagtt ctgtggagct ggaagccaga	60
cctcttttga ggaaactcca gcagctatgt tgggtgtctct gagggaatgc aacaaggctg	120
ctcctccatg tattggaaaa ctgcaactg gactcaactg gaagggaagt ctgctgccag	180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct	240
tcctcctcct gtcatacggg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga	300
g	301

&lt;210&gt; 242

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 242

ccgaggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt	60
tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat	120
gtcttcaaga atatatcatt cctttttcac tagaaccat tcaaatata agtcaagaat	180
cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta	240
taagtaccca aagttttata aatcaaaagc cctaattgata accattttta gaattcaatc	300
a	301

&lt;210&gt; 243

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 243

aggtaagtcc cagtttgaag ctcaaaagat ctggtatgag cataggetca tcgacgacat	60
ggtggcccaa gctatgaaat cagagggagg ctcatctggt gcctgtaaaa actatgatgg	120



tgacgtgcag tcggactctg tggcccaagg gtatggctct ctccggcatga tgaccagcgt 180  
 gctggtttgt ccagatggca agacagtaga agcagaggct gcccacggga ctgtaaccgg 240  
 tcactaccgc atgttccaga aaggacagga gacgtccacc aatcccattg cttccatttt 300  
 t 301

&lt;210&gt; 244

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 244

gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa 60  
 gtcattgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120  
 ccagggacct tggaaacagt tgacactgta aggtgcttgc tccccaagac acatcctaaa 180  
 aggtgttcta atggtgaaaa cgtcttcctt ctttattgcc ctttcttatt tatgtgaaca 240  
 actgtttgtc ttttgtgtat cttttttaa ctgtaaagtt caattgtgaa aatgaatatc 300

&lt;210&gt; 245

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 245

gtctgagtat ttaaaatggt attgaaatta tccccaacca atgttagaaa agaaagaggt 60  
 tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt 120  
 aaggccagga gatattgtca ttaatgtara cttcaggaca cttagagtata gcagccctat 180  
 gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac 240  
 agctaataaa atgaaagacc taatttctaa agcaattctt tataattttac aaagttttaa 300  
 g 301

&lt;210&gt; 246

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 246

ggctctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata 60  
 acctgggctt attttaaaga actatttgta gctcagattg gttttcctat ggctaaaata 120  
 agtgccttct gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac 180  
 taacaatcat actaaatata ttttgaagta caaagtgtga catgctctaa agtgacaacc 240  
 caaatgtgtc ttacaaaaca cgttcctaac aaggatatgt ttacactacc aatgcagaaa 300  
 c 301

&lt;210&gt; 247

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 247

aggtcctttg gcagggtcga tggatcagag ctcaaactgg agggaaaggc atttcgggta 60  
 gcctaagagg gcgactggcg gcagcacaac caaggaaggc aaggttggtt cccccacgct 120  
 gtgtcctgtg ttcaggtgcy acacacaatc ctcatgggaa caggatcacc catgcgctgc 180  
 ccttgatgat caagggtggg gcttaagtgg attaagggag gcaagtcttg ggttccttgc 240  
 cttttcaaac catgaagtca ggctctgtat ccttcctttt cctaactgat attctaacta 300  
 a 301

<210> 248  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 248  
aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60  
attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt 120  
acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180  
gtacattcca gctgtttggc aactccataa aaacatttca gattttaatc ccgaatttag 240  
ctaatagagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300  
c 301

<210> 249  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 249  
gtccagagga agcacctggg gctgaactag gcttgccctg ctgtgaactt gcacttggag 60  
ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtcccgcgc 120  
ccagggagac acagcagtga ctcagagctg gtgcgcacct gtgcctccct cctcaccgcc 180  
catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240  
actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300  
a 301

<210> 250  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 250  
ggctctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc 60  
cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120  
cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac 180  
ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240  
caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300  
a 301

<210> 251  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 251  
gccgaggtcc tacatttggc ccagtttccc cctgcaccc ctcaggggcc cctgcctcat 60  
agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat 120  
ggcagggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180  
cattggggtc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgaa 240  
cctctggagg ggggcagtgg aatcccagct ccaggacgga tcctgtcgaa aagatatcct 300  
c 301

<210> 252  
<211> 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 252

```

gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttctca    60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcatgtcttt caagaatata    120
tcattccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa    180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag tacccaaagt    240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc    300
a

```

301

&lt;210&gt; 253

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 253

```

ttccctaaga agatgttatt ttgttgggtt ttgttccccc tccatctcga ttctcgtacc    60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcccttagct    120
tggtctgatt gttttcagac cttaaaatat aaacttggtt cacaagcttt aatccatgtg    180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt    240
tccatagtgc ccacagggtg ttccctcacat ttctcccata ggaaaatgct ttttcccaag    300
g

```

301

&lt;210&gt; 254

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 254

```

cgctgcgcct ttcccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg    60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaatcccc    120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa    180
gaaaaaataa aagctttgga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc    240
acttaaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc    300
t

```

301

&lt;210&gt; 255

&lt;211&gt; 302

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 255

```

agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa    60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat    120
tgggattttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg    180
aggaaaaagg actggagggt gaattctttt aaaaaacaag agtgattgag gcagattgta    240
aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac    300
aa

```

302

&lt;210&gt; 256

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 256  
gttccagaaa acattgaagg tggcttccca aagtctraact agggataccc cctctagcct 60  
aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc 120  
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat 180  
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt 240  
gtggcctctc ggcctggtta gcaagaacat tcagggtagg cctaagttan tcgtgttagt 300  
t 301

<210> 257  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 257  
gttgtggagg aactctggct tgctcattaa gtcctactga ttttactat cccctgaatt 60  
tccccactta tttttgtctt tcaactatgc aggccttaga agaggtctac ctgcctccag 120  
tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat 180  
gtcacattac tcccttcagt gatttcttgt agaagtgcc atcctgaat gccaccaaga 240  
tcttaattct cacatcttta atcttatctc ttgactcct ctttacaccg gagaaggctc 300  
c 301

<210> 258  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 258  
cagcagtagt agatgccgta tgccagcag cccagcactc ccaggatcag caccagcacc 60  
aggggcccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120  
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg 180  
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240  
tggtgatccc tgggagcgcc ggtggagtaa cgttggcca tggaaagcag cgcccacaac 300  
t 301

<210> 259  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 259

```

tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg      60
gtgtcctgaa gtgatttga cccctgaggg cagacaccta agtaggaatc ccagtgggaa      120
gcaaagccat aaggaagccc aggattcctt gtgacagga agtggggccag gaaggtctgt      180
tccdgctcac atctcatctg catgcagcac ggaccggatg cggccactgg gtcttggctt      240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcatecttgg ctccaggtgg      300
c                                                                           301

```

```

<210> 260
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 260
ttttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaa at aagcaatggt      60
aaggtgtctt aacttgaaaa agattaggag tctctggtt acaagttata attgaatgaa      120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaaca caggattaac      180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttaataaac agactgattc      240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca      300
c                                                                           301

```

```

<210> 261
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 261
aaatattcga gcaaatcctg taactaatgt gtctccataa aaggctttga actcagtga      60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaaggtt      120
agcaccaact attccataca attcatcagc aggaaataaa ggctcttcag aaggttcaat      180
ggtgacatcc aatttcttct gataatttag attcttcaca accttcttag ttaagtgaag      240
ggcatgatga tcattcaaag cccagtggtc acttactcca gactttctgc aatgaagatc      300
a                                                                           301

```

```

<210> 262
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 262
gaggagagcc tggtacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc      60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaattc ctgagtcacc      120
cctagacttc ctaaaccaga tctctgggg ctggaacctg gcactctgca tttgtaatga      180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtggcc      240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat      300
c                                                                           301

```

```

<210> 263
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (301)
<223> n = A,T,C or G

```

## &lt;400&gt; 263

tttagcttgt	ggtaaatgac	tcacaaaact	gatttttaaaa	tcaagttaat	gtgaattttg	60
aaaattacta	cttaatccta	attcacaata	acaatggcat	taaggtttga	cttgagttgg	120
ttcttagtat	tatttatggg	aaataggctc	ttaccacttg	caaataactg	gccacatcat	180
taatgactga	cttcccagta	aggctctcta	aggggttaagt	angaggatcc	acaggatttg	240
agatgctaag	gccccagaga	tcgtttgatc	caacctctct	attttcagag	gggaaaatgg	300
g						301

&lt;210&gt; 264

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 264

aaagacgtta	aaccactcta	ctaccacttg	tggaactctc	aaagggtaaa	tgacaaaacc	60
aatgaatgac	tctaaaaaca	atatttacat	ttaatggttt	gtagacaata	aaaaaacaag	120
gtggatagat	ctagaattgt	aacattttta	gaaaaccata	scatttgaca	gatgagaaag	180
ctcaattata	gatgcaaagt	tataactaaa	ctactatagt	agtaaagaaa	tacatttcac	240
acccttcata	taaattcact	atcttggtt	gaggcactcc	ataaaatgta	tcacgtgcac	300
a						301

&lt;210&gt; 265

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 265

tgcccaagtt	atgtgtaagt	gtatccgcac	ccagaggtaa	aactacactg	tcattcttct	60
cttcttctga	cgcagtatct	cttctctggg	gagaagccgg	gaagtcttct	cctggctcta	120
catattcttg	gaagtctcta	atcaactttt	gttccatttg	tttcatttct	tcaggaggga	180
ttttcagttt	gtcaacatgt	tctctaacaa	cacttgccca	tttctgtaaa	gaatccaaag	240
cagtccaagg	ctttgacatg	tcaacaacca	gcataactag	agtatccttc	agagatacgg	300
c						301

&lt;210&gt; 266

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 266

taccgtctgc	ccttctctcc	atccaggcca	tctgcgaatc	tacatgggtc	ctcctattcg	60
acaccagatc	actctttcct	ctaccacacag	gcttgctatg	agcaagagac	acaacctcct	120
ctcttctgtg	ttccagcttc	tttctctgtt	cttcccaccc	cttaagtctc	attcctgggg	180
atagagacac	caatacccat	aacctctctc	ctaagcctcc	ttataaccca	gggtgcacag	240
cacagactcc	tgacaactgg	taaggccaat	gaactgggag	ctcacagctg	gctgtgcctg	300
a						301

&lt;210&gt; 267

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

## &lt;400&gt; 267

aaagagcaca	ggccagctca	gcctgccctg	gccatctaga	ctcagcctgg	ctccatgggg	60
------------	------------	------------	------------	------------	------------	----

gtttctcagtg ctgagtccat ccaggaaaag ctcacctaga ccttctgagg ctgaatcttc 120  
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatggctt ggagtaaagc 180  
ctcattctga ttcctctcct tcttttcttt caagttggct ttcctcacat cctctgttc 240  
aattcgcttc agcttgctg ctttagccct catttccaga agcttcttct ctttggcattc 300  
t 301

<210> 268  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 268  
aatgtctcac tcaactactt cccagcctac cgtggccta tcttgggagt tttcttctta 60  
gatcttggga gagctggctt ttctaaggag aaggaggaag gacagatgta actttggatc 120  
tcgaagagga agtctaattg aagtaattag tcaacggctc ttgtttagac tcttggata 180  
tgctgggtgg ctcatgagc ccttttggag aaagcaagta ttattcttaa ggagtaacca 240  
cttcccattg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact 300  
a 301

<210> 269  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 269  
taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60  
aaaattacct ttattcacac atctcaaac aattctgcaa attcttagtg aagtttaact 120  
atagtcacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta 180  
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta 240  
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300  
t 301

<210> 270  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 270  
cattgaagag cttttgcgaa acatcagaac acaagtgtt ataaaattaa ttaagcctta 60  
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120  
gagcttgctg gtgcagtga tattggataa cactattcat ggccgaattg atcaagtcaa 180  
ccaactcctt gaactggatc atcagaagaa ggggtgtgca cgatatactg cactagataa 240  
tggaaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300  
a 301

<210> 271  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)... (301)  
<223> n = A,T,C or G

&lt;400&gt; 271

```
aaaagggtct cataagatta acaattttaa taaatatttg atagaacatt ctttctcatt    60
tttatagctc atcttttagg ttgatattca gtccatgctt cccttgctgt tcttgatcca    120
gaattgcaat cacttcatca gcctgtattc gctccaattc tctataaagt ggggtccaagg    180
tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt    240
tctctctccc agatganaac tgatcatgcg cccacatttt ggggttttata gaagcagtca    300
c
```

&lt;210&gt; 272

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 272

```
taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaattgtc    60
ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga    120
tccaataatt ccttcatgat gagcaagaaa aattcttttg gcacccctcc tgcattccaca    180
gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgttttc    240
ctaaggactt ccattgcatc tcctacaata ttttctctac gcaccactag aattaagcag    300
g
```

&lt;210&gt; 273

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 273

```
acatgtgtgt atgtgtatct ttgggaaaaan aanaagacat cttgtttayt atttttttgg    60
agagangctg ggacatggat aatcacwtaa ttgctayta tyactttaat ctgactygaa    120
gaaccgtcta aaaataaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc    180
tlytttctgt ccagagagag tatcagtgac ananatttma ggggtgaamac atgmattggt    240
gggacttnty tttacngagm accctgcccc sgcgccctcg makcngantt ccgcsananc    300
t
```

&lt;210&gt; 274

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) ... (301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 274

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cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg    60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa    120
tgatttctct tggaaatctga atgagatcaa gaggccagct ttagcttgtg gaaaagtcca    180
tctaggtagt gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc    240
aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaaagt    300
```



c

301

<210> 275  
<211> 301  
<212> DNA  
<213> Homo sapien  
  
<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 275  
tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60  
gggtgaaatt ggccaacttt ctattaactt atgttggaat ttttgccacc aacagtaagc 120  
tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag 180  
tcaagagact ccagggcctc agcgtacctg cccggggcgg cgctcgaagc cgaattctgc 240  
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccttat 300  
a 301

<210> 276  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 276  
tgtacacata ctcaataaat aaatgactgc attgtgggtat tattactata ctgattatat 60  
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat 120  
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180  
caatacatctt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttctgt 240  
aaaactattc agtatgttcc ccttgcttca tgtctgagaa ggctctcctt caatggggat 300  
g 301

<210> 277  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 277  
tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60  
atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120  
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgccccca cctcgtcctt 180  
caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga 240  
gttcnctgic gattacatct gaccagtctc ctttttccga agtcctntccg ttcaatcttg 300  
c 301

<210> 278  
<211> 301  
<212> DNA  
<213> Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 278

taccactaca	ctccagcctg	ggcaacagag	caagacctgt	ctcaaagcat	aaaatggaat	60
aacatatcaa	atgaaacagg	gaaaatgaag	ctgacaattt	atggaagcca	gggcttgta	120
cagtctctac	tggtattatg	cattacctgg	gaatttatat	aagcccttaa	taataatgcc	180
aatgaacatc	tcatgtgtgc	tcacaatggt	ctggcactat	tataagtgtc	tcacagggtt	240
tatgtgttct	tcgtaacttt	atggantagg	tactcggccg	cgaacacgct	aagccgaatt	300
c						301

&lt;210&gt; 279

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 279

aaagcaggaa	tgacaaagct	tgcttttctg	gtatgttcta	ggtgtattgt	gacttttact	60
gttatattaa	ttgccaatat	aagtaaatat	agattatata	tgtatagtgt	ttcacaaagc	120
ttagaccttt	accttccagc	cacccacag	tgcttgatat	ttcagagtca	gtcattgggt	180
atacatgtgt	agttccaaag	cacataagct	agaanaanaa	atatttctag	ggagcactac	240
catctgtttt	cacatgaaat	gccacacaca	tagaactcca	acatcaattt	cattgcacag	300
a						301

&lt;210&gt; 280

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 280

ggtactggag	ttttcctccc	ctgtgaaaac	gtaactactg	ttgggagtga	attgaggatg	60
tagaaagggt	gtggaaccaa	attgtgggtc	atggaaatag	gagaatatgg	ttctcactct	120
tgagaaaaaa	acctaaagatt	agcccaggta	gttgccgtga	acttcagttt	ttctgcctgg	180
gtttgatata	gtttagggtt	gggggttagat	taagatctaa	attacatcag	gacaaagaga	240
cagactatta	actccacagt	taattaagga	ggtatgttcc	atgtttattt	gttaaagcag	300
t						301

&lt;210&gt; 281

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 281

aggtacaaga	aggggaatgg	gaaagagctg	ctgctgtggc	attgttcaac	ttggatatcc	60
gccgagcaat	ccaaatcctg	aatgaagggg	catcttctga	aaaaggagat	ctgaatctca	120
atgtggtagc	aatggcttta	tcgggttata	cggatgagaa	gaactccctt	tggagagaaa	180
tgtgtagcac	actgcgatta	cagctaaata	acccgtattt	gtgtgtcatg	tttgcatttc	240

tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagtt gcagtacctc 300  
g 301

<210> 282

<211> 301

<212> DNA

<213> Homo sapien

<400> 282

caggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60  
tccagaacct aaaaattaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120  
agcgcagaag caaagcccag gcagaacctat gctaacccta cagctcagcc tgcacagaag 180  
cgcagaagca aagcccaggc agaacctatg taaccttaca gctcagcctg cacagaagcg 240  
cagaagcaaa gcccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300  
a 301

<210> 283

<211> 301

<212> DNA

<213> Homo sapien

<400> 283

atctgtatag ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60  
cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120  
gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180  
acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcattcttta 240  
ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300  
g 301

<210> 284

<211> 301

<212> DNA

<213> Homo sapien

<400> 284

caggtacaaa acgctattaa gtggcttaga atttgaacat ttgtggctct tatttacttt 60  
gcttcgtgtg tgggcaaagc aacatcttcc cttaatatat attaccaaga aaagcaagaa 120  
gcagattagg tttttgacaa aacaaacagg ccaaaagggg gctgacctgg agcagagcat 180  
ggtgagaggc aaggcatgag agggcaagtt tggtgtggac agatctgtgc ctactttatt 240  
actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300  
a 301

<210> 285

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 285

acatcaccat gatcggatcc cccaccatt atacgttgta tgtttacata aatactcttc 60  
aatgatcatt agtgttttta aaaaaatact gaaaactcct tctgcatccc aatctctaac 120

caggaaagca aatgctatctt acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180  
attaaatatg tctgacttct tttgaggta cactgactagg caaatgctat ttacgatctg 240  
caaaagctgt ttgaagagtc aaagcccca tgtgaacacg atttctggac cctgtaacag 300  
t 301

<210> 286  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 286  
taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaa aaactttgct 60  
tgtatatat ttttgcctta cagtggatca ttctagtagg aaaggacagt aagatttttt 120  
atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccacca 180  
aaaataagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt 240  
gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg 300  
t 301

<210> 287  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 287  
tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgtggg 60  
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg 120  
aaatgatttg gttatgaacg cacagttagg gcagcagggc cagaatcctg accctctgcc 180  
ccgtgggtat ctctcccca gcttggctgc ctcatgttat cacagtattc cattttgttt 240  
gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc 300  
t 301

<210> 288  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 288  
gtacaccta ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60  
agtcaatagg aagacaaatt ccagttccag ctcatctggt gtatctgcaa agctgcaaaa 120  
gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180  
aaaagcatct gcttttgtga ttttaatttag ctcatctggc cactggaaga atccaaacag 240  
tctgccttaa ttttggatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300  
a 301

<210> 289  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 289

60  
120  
180  
240  
300  
301

```
<220>  
<221> misc_feature  
<222> (1)...(301)  
<223> n = A,T,C or G
```

60  
120  
180  
240  
300  
301

<400> 291

60  
120  
180  
240  
300  
301

```
<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G
```

60  
120  
180  
240  
300  
301

<210> 293  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 293  
 ggtaccaagt gctggtgccg gcctgttacc tgtttctact gaaaagtctg gctaattgctc 60  
 ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcttagagc actgactgtt 120  
 aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt 180  
 gtgagaattt tttaaaaggc tacttgata ataacccttg tcatttttaa tgtacctcgg 240  
 ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300  
 g 301

<210> 294  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 294  
 tgacccataa caatatacac tagctatctt ttttaactgtc catcattagc accaatgaag 60  
 attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag 120  
 ttttaactata gtcacaganc ttaaattatc acattgtttt ctatgtctac tgaaaataag 180  
 ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240  
 cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt 300  
 t 301

<210> 295  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 295  
 gtactctttt tctccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60  
 cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120  
 ttgggtttgt aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180  
 actggtagaa aaacrtctga agagctagtc tatcagcatc tgacaggtga attggatggg 240  
 tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300  
 tctct 305

<210> 296  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 296  
 aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct 60  
 cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120  
 attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180  
 tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240

tgccattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300  
c 301

<210> 297

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 297

actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60  
aaggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga 120  
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180  
tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc 240  
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc acactggcgg 300

<210> 298

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 298

tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc cctcccgcg 60  
ggcatctgag agacctggtg tccagtgtt tctggaaatg ggtcccagtg ccgccggctg 120  
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccacctt 180  
gtcctgtctg ttacatttc actaycaggc tttctctggg cattacnatt tgttccccta 240  
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcagggtggc ctcagcgagg 300  
t 301

<210> 299

<211> 301

<212> DNA

<213> Homo sapien

<400> 299

gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc 60  
tcaactgcacc ctctgcctcc cagggttcgag caattctcct gcctcagcct cccaggtagc 120  
tgggattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg 180  
gagtttcgcc atgttggcca gctgggtctca aactcctgac ctcaagcgac ctgcctgcct 240  
cggcctccca aagtgtctga attataggca tgagtcaaca cgcccagcct aaagatatatt 300  
t 301

<210> 300

<211> 301

<212> DNA

<213> Homo sapien

&lt;400&gt; 300

attcagtttt atttgctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60  
tatgtccac acccactggg aaaggctccc acctggctac ttctctatc agctgggtca 120  
gctgcattcc acaaggttct cagcctaata agtttacta cctgccagtc tcaaaactta 180  
gtaaagcaag accatgacat tccccacgg aatcagagt ttgccccacc gtcttggtac 240  
tataaagcct gcctctaaca gtccttgctt cttcacacca atccccgagc catcccccat 300  
g 301

&lt;210&gt; 301

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 301

ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60  
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt 120  
gggaactcac aaagaccctc agagctgaga caccacacac agtgggagct cacaaagacc 180  
ctcagagctg agacaccac aacagtggga gtcacaaaag accctcagag ctgagacacc 240  
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300  
t 301

&lt;210&gt; 302

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 302

aggtacacat ttagcttggt gtaaataact cacaataact attttaaaat caagttaatg 60  
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac 120  
ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg 180  
ccacatcatt aatgactgac tccccagtaa ggctctctaa ggggtaagta ggaggatcca 240  
caggatttga gatgctaagg cccagagat cgtttgatcc aacctctta ttttcagagg 300  
g 301

&lt;210&gt; 303

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 303

aggtaccaac tgtggaaata ggtagaggat cttttttct tccatatca actaagttgt 60  
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac 120  
tggctaattg aactaccgct tgcattgtaa aaatgggtgt ttgtgaaatg atcataggcc 180  
agtaacgggt atgtttttct aactgatctt ttgtcgttc caaagggacc tcaagacttc 240  
catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac 300  
c 301

&lt;210&gt; 304

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 304

acatggatgt tttttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaatt 60



```

tattagtttc agtttcagct taccacttt ttgtctgcaa catgcaraas agacagtgcc      120
cttttttagtg tatcatatca ggaatcatct cacattgggt ttgtgccatta ctgggtgcagt    180
gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga     240
ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct    300
c                                                                           301

```

&lt;210&gt; 305

&lt;211&gt; 301

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(301)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 305

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gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag      60
caggggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggcg    120
taaaggagga gaaacagata caaaatctcc aactcagtat taaggatttc tcatgcctag    180
aatattggta gaaacaagaa tacattcata tggcaaataa ctaaccatgg tggaacaaaa     240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag    300
a                                                                           301

```

&lt;210&gt; 306

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 306

```

Val Leu Gly Trp Val Ala Glu Leu
1           5

```

&lt;210&gt; 307

&lt;211&gt; 637

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 307

```

acaggggratg aaggsgaaagg gagaggatga ggaagccccc ctggggattt ggtttgggtcc      60
ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa atagggggcac    120
attgaggaat gatacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt    180
cacaccattg gtgagggagg gattaccacc ctgggggttat gaagatggtt gaacacccca    240
cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga    300
gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattggtgtg    360
aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacgggtggg caaactctga    420
tttccgtggg ggaatgtcat ggtcttgctt tactaagttt tgagactggc aggtagttaa    480
actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca    540
gggtgggagcc tttcccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg    600
ttacagatac tggggcagca aataaaactg aatctttg                                     637

```

&lt;210&gt; 308

&lt;211&gt; 647

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(647)  
 <223> n = A,T,C or G

<400> 308

acgattttca ttatcatgta aatcgggtca ctcaaggggc caaccacagc tgggagccac	60
tgctcagggg aaggttcata tgggactttc tactgccccaa gggtctatac aggatataaa	120
ggngcctcac agtatagatc tggtagcaaa gaagaagaaa caaacactga tctctttctg	180
ccaccctct gaccctttgg aactcctctg acccttttaga acaagcctac ctaatatctg	240
ctagagaaaa gaccaacaac ggcctcaaag gatctcttac catgaagggtc tcagctaatt	300
cttgggctaag atgtgggttc cacattaggt tctgaatatg gggggaagg tcaatttgct	360
cattttgtgt gtggataaag tcaggatgcc cagggggccag agcagggggc tgcttgcttt	420
gggaacaatg gctgagcata taaccatagg ttatggggaa caaaacaaca tcaaagtcac	480
tgatcaatt gccatgaaga cttgagggac ctgaatctac cgattcatct taaggcagca	540
ggaccagttt gagtggcaac aatgcagcag cagaatcaat ggaaacaaca gaatgattgc	600
aatgtccttt tttttctcct gcttctgact tgataaaagg ggaccgt	647

<210> 309  
 <211> 460  
 <212> DNA  
 <213> Homo sapien

<400> 309

actttatagt ttaggctgga cattggaaaa aaaaaaagc cagaacaaca tgtgatagat	60
aatatgattg gctgcacact tccagactga tgaatgatga acgtgatgga ctattgtatg	120
gagcacatct tcagcaagag ggggaaatac tcatcatttt tggccagcag ttgtttgatc	180
accaaacatc atgccagaat actcagcaaa ccttcttagc tcttgagaag tcaaagtcag	240
ggggaattta ttcctggcaa ttttaattgg actccttagt tgagagcagc ggctaccag	300
ctgggggtgg ggagcgaacc cgtcactagt ggacatgcag tggcagagct cctggtaacc	360
acctagagga atacacaggc acatgtgtga tgccaagcgt gacacctgta gcactcaaat	420
ttgtcttgtt tttgtctttc sgtgtgtaag attcttaagt	460

<210> 310  
 <211> 539  
 <212> DNA  
 <213> Homo sapien

<400> 310

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taggaagag aaacacagaa ggaagagaca caataaaagt cattatgtat tctgtgagaa	180
gtcagacagt aagatttgtg ggaatgggt tggtttgttg tatggtatgt attttagcaa	240
taatctttat ggcagagaaa gctaaaatcc tttagcttgc gtgaatgatc acttgctgaa	300
ttcctcaagg taggcatgat gaaggagggt ttagaggaga cacagacaca atgaactgac	360
ctagatagaa agccttagta tactcagcta ggaatagtga ttctgagggc acactgtgac	420
atgattatgt cattacatgt atggtagtga tggggatgat aggaaggaag aacttatggc	480
atattttcac ccccaaaaa gtcagttaaa tattgggaca ctaaccatcc aggtcaaga	539

<210> 311  
 <211> 526  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(526)  
 <223> n = A,T,C or G

<400> 311  
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 catttacagc atttaaaatg tgttcagcat gaaatattag ctacagggga agctaaataa 180  
 attaaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg 240  
 tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa 300  
 aaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc 360  
 tctctttaca gggagctcct gcagcccta cagaaatgag tggctgagat tcttgattgc 420  
 acagcaagag cttctcatct aaacctttc cctttttagt atctgtgtat caagtataaa 480  
 agttctataa actgtagtnt acttatttta atcccaaaag cacagt 526

<210> 312  
 <211> 500  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(500)  
 <223> n = A,T,C or G

<400> 312  
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 tcatttctga aagcagttga gccactttat tccaaagtag actgcagatg ttcaaactct 120  
 ccatttctct ttcccttcca cctgccagtt ttgctgactc tcaacttgct atgagtgtaa 180  
 gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg 240  
 gcttcttagg aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atccccctt 300  
 tgcagatgct tagcagcttc agacatttgg ttaagaacct atgggaaaaa aaaaaatcct 360  
 tgctaattgt gtttctttg taaaccanga ttcttatttg nctgggtatag aatatcagct 420  
 ctgaacgtgt ggtaaagatt ttgtgtttg aatataggag aaatcagttt gctgaaaagt 480  
 tagtcttaat tatctattgg 500

<210> 313  
 <211> 718  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(718)  
 <223> n = A,T,C or G

<400> 313  
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 ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa 180  
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 aaaaaggaa acagagatcc ctgggagaaa tggccggccg ccatcttggg tcatcgatga 300  
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 ttccttaaag gatggcagga aaacagatcc tgtgtggat atttatttga acgggattac 420

agatttgaaa tgaagtcaca aagtgagcat taccaatgag aggaaaacag acgagaaaat	480
cttgatgggt cacaagacat gcaacaaaca aaatggaata ctgtgatgac acgagcagcc	540
aactggggag gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg	600
cggtatacca atcattttcta tttctaccct caaacaagct gtngaataac tgacttacgg	660
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&lt;210&gt; 314

&lt;211&gt; 358

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 314

gtttatttac attacagaaa aaacatcaag acaatgtata ctatttcaaa tatatccata	60
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caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa	180
gctctcggtg gtccagccac tgtgaaacat gtcctcttta gattaacctc gtggacgctc	240
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&lt;210&gt; 315

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 315

taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc	60
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gacccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag cccaatgac	180
agtcaccagc tccccgacca gccggatata gtccttaggg gtcatgtagg ctccctgaag	240
tagcttctgc tgtaagaggg tgttgctccc ggggctcgtg cggttattgg tccctgggctt	300
gagggggcgg tagatgcagc acatggtgaa gcagatgatg t	341

&lt;210&gt; 316

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 316

agactgggca agactcttac gccccacact gcaatttggt cttgttgccg tatccattta	60
tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact	120
cattcagggg gctctgggtg caatattagt t	151

&lt;210&gt; 317

&lt;211&gt; 151

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 317

agaactagtg gatcctaag aaatacctga aacatatatt ggcatttata aatggctcaa	60
atcttcattt atctctggcc ttaacctgg ctcctgaggg tgcggccagc agatcccagg	120
ccagggtctt gttcttgcca cactgcttg a	151

&lt;210&gt; 318

&lt;211&gt; 151

&lt;212&gt; DNA

<213> Homo sapien

<400> 318

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actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcgga gggacctcct    60
gctgcaggct ggagtgtctt tttcctggc gggagaccgc acattccact gctgaggctg    120
tggtggcggt ttatcaggca gtgataaaca t                                  151
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<210> 319

<211> 151

<212> DNA

<213> Homo sapien

<400> 319

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catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg    120
taagattggg tttatgtgat tttagtgggt a                                  151
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<210> 320

<211> 150

<212> DNA

<213> Homo sapien

<400> 320

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gagcggctgc cttttttttt tttttttttg ggggggaatt tttttttttt aatagttatt    120
gagtgttcta cagcttacag taaataccat                                  150
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<210> 321

<211> 151

<212> DNA

<213> Homo sapien

<400> 321

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tgctctgag aaatcaaagt cttcatacac t                                  151
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<210> 322

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 322

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tttgggcttg gtcagtttgc cacagggctt ggagatgggt acagtcttct ggcattcggc    120
attgtgcagg gctcgcttca nacttccagt t                                  151
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<210> 323

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

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nagactcant tactaccag tttgtggtt twtgggagaa atgtaactgg acagttagct	120
gttcaatyaa aaagacactt ancccatgtg g	151

<210> 324

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 324

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agagttacta cgaatcccat cttggttcca gctatatcac tgacagcatg gtagaagact	180
gcgaacctca cttctagact ttacgggtgg gacgaaacgg gtccagaaac tgcaggggc	240
ctcatacagg gatataaaa taccctttgt gctaccagg cctggggaa tcagggtgact	300
cacacaaatg caatagtgg tcaactgcatt ttacctgaa ccaaagctaa acccgggtgt	360
gccaccatgc accatggcat gccagagttc aacactgttg ctcttgaaaa ttgggtctga	420
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<210> 325

<211> 400

<212> DNA

<213> Homo sapien

<400> 325

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agtaagagtg gtggcctatt tcagctgctt tgacaaaaatg actggctcct gacttaacgt	180
tctataaatg aatgtgctga agcaaagtgc ccatgggtggc ggcgaagaag agaaagatgt	240
gttttgtttt ggactctctg tgggtccctc caatgctgtg gggttccaac caggggaagg	300
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<210> 326

<211> 1215

<212> DNA

<213> Homo sapien

<400> 326

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gaactcctac accatcgggc tgggctgca cagtcttgag gccgaccaag agccaggcag	180

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aaaaaaaaa aaaaaa 1215

```

&lt;210&gt; 327

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 327

```

Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
1      5      10      15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
20     25     30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
35     40     45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
50     55     60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
65     70     75     80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
85     90     95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
100    105    110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
115    120    125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
130    135    140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
145    150    155    160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
165    170    175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
180    185    190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
195    200    205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
210    215    220

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&lt;210&gt; 328

<211> 234  
 <212> DNA  
 <213> Homo sapien

<400> 328  
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 atccgcagtg ggtgctgtca gccacacact gtttccagaa ctctacacc atcgggctgg 180  
 gcctgcacag tcttgaggcc gaccaagagc caggagacca gatggtggag gcca 234

<210> 329  
 <211> 77  
 <212> PRT  
 <213> Homo sapien

<400> 329  
 Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser  
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 Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu  
 20 25 30  
 Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr  
 35 40 45  
 His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu  
 50 55 60  
 Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala  
 65 70 75

<210> 330  
 <211> 70  
 <212> DNA  
 <213> Homo sapien

<400> 330  
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 gctgcagcca 70

<210> 331  
 <211> 22  
 <212> PRT  
 <213> Homo sapien

<400> 331  
 Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu  
 1 5 10 15  
 Val Ser Gly Ser Cys Ser  
 20

<210> 332  
 <211> 2507  
 <212> DNA  
 <213> Homo sapien

<400> 332  
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 tgcccttcc tctgtatatg gctgcgcccc aaatcaggaa aatgctgtcc agtgggggtc 120



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&lt;210&gt; 333

&lt;211&gt; 3030

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 333

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&lt;210&gt; 334

&lt;211&gt; 2417

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 334

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&lt;211&gt; 2984

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 335

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&lt;210&gt; 336

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 336

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20          25          30
Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
35          40          45
Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
50          55          60
Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
65          70          75          80

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Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln  
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 Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala  
                   100                  105                  110  
 Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn  
                   115                  120                  125  
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 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys  
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 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala  
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 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu

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                                  195                      200                      205  
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 Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe  
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                                  260                      265                      270  
 Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His  
                                  275                      280                      285  
 Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg  
                                  290                      295                      300  
 Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp  
 305                                   310                      315

&lt;210&gt; 340

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 340

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&lt;210&gt; 341

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 341

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&lt;210&gt; 342

&lt;211&gt; 592

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 342

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&lt;210&gt; 343

&lt;211&gt; 382

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 343

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&lt;210&gt; 344

&lt;211&gt; 536

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 344

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&lt;210&gt; 345

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 345

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actcctgggt t

251

&lt;210&gt; 350

&lt;211&gt; 908

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 350

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&lt;210&gt; 351

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 351

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&lt;210&gt; 352

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 352

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&lt;210&gt; 353

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 353

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&lt;210&gt; 354

&lt;211&gt; 854

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 354

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&lt;210&gt; 355

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 355

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&lt;210&gt; 356

&lt;211&gt; 574

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 356

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&lt;210&gt; 357

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 357

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&lt;210&gt; 358

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 358

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&lt;210&gt; 359

&lt;211&gt; 620

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 359

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&lt;210&gt; 360

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 360

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&lt;210&gt; 361

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 361

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&lt;210&gt; 362

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 362

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&lt;210&gt; 363

&lt;211&gt; 653

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(653)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 363

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&lt;210&gt; 364

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 364

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&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 365

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&lt;210&gt; 366

&lt;211&gt; 1851

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 366

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&lt;210&gt; 367

&lt;211&gt; 668

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 367

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668

&lt;210&gt; 368

&lt;211&gt; 1512

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 368

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&lt;210&gt; 369

&lt;211&gt; 1853

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 369

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&lt;210&gt; 370

&lt;211&gt; 2184

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 370

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<210> 371  
<211> 1855  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(1855)  
<223> n = A,T,C or G

<400> 371

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<210> 372  
<211> 1059  
<212> DNA  
<213> Homo sapien

<400> 372

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gcgcttgrgg agactmcgat gacagygcct tcatggagcc caggtaccac gtcctgtagg      180
aagatctgga caagctccac agagctgccc tgggtgggta aagctcccag aaaggatctc     240
atcgtcatgc tcagggacac tgaygtgaac aagarggaca agcaaaagag gactgctcta     300
catctggcct ctgccaatgg gaattcagaa gtagtaaaac tcctgctgga cagacgatgt     360
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&lt;210&gt; 373

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 373

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&lt;210&gt; 374

&lt;211&gt; 2000

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 374

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aaacagatgc	caaaatactc	ttctgaaaac	agcaaccag	aacaagactt	aaagctgaca	1500
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ctgactaatg	gtgccactgc	tggcaatggt	gatgatggat	taattcctcc	aagggaagagc	1680
agaacacctg	aaagccagca	atttcctgac	actgagaatg	aagagtatca	cagtgcagaa	1740
caaaatgata	ctcagaagca	attttctgaa	gaacagaaca	ctggaatatt	acacgatgag	1800
attctgattc	atgaagaaaa	gcagatagaa	gtgggtgaaa	aaatgaattc	tgagctttct	1860
cttagttgta	agaaagaaaa	agacatcttg	catgaaaata	gtacgttgcg	ggaagaaatt	1920
gccatgctaa	gactggagct	agacacaatg	aaacatcaga	gccagctaaa	aaaaaaaaaa	1980
aaaaaaaaaa	aaaaaaaaaa					2000

&lt;210&gt; 375

&lt;211&gt; 2040

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 375

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aggagcaaga	tgggcaagtg	gtgctgccgt	tgcttcccc	gctgcaggga	gagcggcaag	120
agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	ggtgccgcca	ctgcttcccc	tgctgcaggg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tgggtgctgc	actgttcccc	ctgctgcagg	gggagcggca	agagcaaggt	gggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccagggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctggtggggt	aaagtcccca	gaaaggatct	catcgtcatg	480
ctcagggaaca	ctgacgtgaa	caagaaggac	aagcaaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgatg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcca	ggaagatgaa	660
tgtgcgtaa	tgttgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
tatgggtgctg	atatcgaatc	aaaaaacaag	catggcctca	caccactgtt	acttgggtgta	840
catgagcaaa	aacagcaagt	cgtgaaatct	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgctgtat	gttggtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggacagacg	1020
gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctcttct	gaaaacagca	atccagaaca	agacttaaaag	1140
ctgacatcag	aggaagagtc	acaaagggtc	aaaggcagtg	aaaatagcca	gccagagaaa	1200
atgtctcaag	aaccagaaat	aaataaggat	ggtgatagag	agggtgaaga	agaaatgaag	1260
aagcatgaaa	gtaataatgt	gggattacta	gaaaacctga	ctaattggtgt	cactgctggc	1320
aatgggtgata	atggattaat	tcctcaaagg	aagagcagaa	cacctgaaaa	tcagcaattt	1380

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cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa 1440
aaacagatgc caaaatactc ttctgaaaac agcaacccag aacaagactt aaagctgaca 1500
tcagaggaag agtcacaaag gcttgagggc agtgaaaatg gccagccaga gaaaagatct 1560
caagaaccag aaataaataa ggatggtgat agagagctag aaaattttat ggctatcgaa 1620
gaaatgaaga agcacggaag tactcatgtc ggattcccag aaaacctgac taatggtgcc 1680
actgctggca atggtgatga tggattaatt cctccaagga agagcagaac acctgaaagc 1740
cagcaatttc ctgacactga gaatgaagag tatcacagtg acgaacaaaa tgatactcag 1800
aagcaatttt gtgaagaaca gaacactgga atattacacg atgagattct gattcatgaa 1860
gaaaagcaga tagaagtggc tgaaaaaatg aattctgagc tttctcttag ttgtaagaaa 1920
gaaaaagaca tcttgcatga aaatagtacg ttgcgggaag aaattgccat gctaagactg 1980
gagctagaca caatgaaaca tcagagccag ctaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040

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&lt;210&gt; 376

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 376

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Met Asp Ile Val Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe
 1          5          10          15
Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
 20          25          30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
 35          40          45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Arg Gly His Phe Trp Arg
 50          55          60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
 65          70          75          80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
 85          90          95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100          105          110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115          120          125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
130          135          140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145          150          155          160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
165          170          175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
180          185          190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
195          200          205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
210          215          220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225          230          235          240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
245          250          255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
260          265          270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
275          280          285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu

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290 295 300  
 Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu  
 305 310 315 320  
 Ser Met Leu Phe Leu Val Ile Ile Met  
 325

<210> 377  
 <211> 148  
 <212> PRT  
 <213> Homo sapien

<220>  
 <221> VARIANT  
 <222> (1)...(148)  
 <223> Xaa = Any Amino Acid

<400> 377  
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 1 5 10 15  
 Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys  
 20 25 30  
 Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys  
 35 40 45  
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu  
 50 55 60  
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp  
 65 70 75 80  
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp  
 85 90 95  
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro  
 100 105 110  
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp  
 115 120 125  
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser  
 130 135 140  
 Lys Asn Lys Val  
 145

<210> 378  
 <211> 1719  
 <212> PRT  
 <213> Homo sapien

<400> 378  
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1 5 10 15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 20 25 30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn



Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp  
 530 535 540  
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln  
 545 550 555 560  
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val  
 565 570 575  
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn  
 580 585 590  
 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu  
 595 600 605  
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp  
 610 615 620  
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys  
 625 630 635 640  
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys  
 645 650 655  
 Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys  
 660 665 670  
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala  
 675 680 685  
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly  
 690 695 700  
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser  
 705 710 715 720  
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser  
 725 730 735  
 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln  
 740 745 750  
 Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys  
 755 760 765  
 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser  
 770 775 780  
 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp  
 785 790 795 800  
 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly  
 805 810 815  
 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn  
 820 825 830  
 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe  
 835 840 845  
 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser  
 850 855 860  
 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn  
 865 870 875 880  
 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu  
 885 890 895  
 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile  
 900 905 910  
 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn  
 915 920 925  
 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro  
 930 935 940  
 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu  
 945 950 955 960  
 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe

	965		970		975
Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His					
	980		985		990
Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser					
	995		1000		1005
Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu					
	1010		1015		1020
Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His					
	1025		1030		1035
Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met					
	1045		1050		1055
Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met					
	1060		1065		1070
Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys					
	1075		1080		1085
Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr					
	1090		1095		1100
Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys					
	1105		1110		1115
Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp					
	1125		1130		1135
Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His					
	1140		1145		1150
Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp					
	1155		1160		1165
Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg					
	1170		1175		1180
Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val					
	1185		1190		1195
Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys					
	1205		1210		1215
Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly					
	1220		1225		1230
Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn					
	1235		1240		1245
Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys					
	1250		1255		1260
Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro					
	1265		1270		1275
Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr					
	1285		1290		1295
Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp					
	1300		1305		1310
Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val					
	1315		1320		1325
His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala					
	1330		1335		1340
Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala					
	1345		1350		1355
Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn					
	1365		1370		1375
Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr					
	1380		1385		1390
Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr					
	1395		1400		1405



Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu  
 1410 1415 1420  
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly  
 1425 1430 1435 144  
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn  
 1445 1450 1455  
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser  
 1460 1465 1470  
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly  
 1475 1480 1485  
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu  
 1490 1495 1500  
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys  
 1505 1510 1515 152  
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser  
 1525 1530 1535  
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu  
 1540 1545 1550  
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser  
 1555 1560 1565  
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe  
 1570 1575 1580  
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe  
 1585 1590 1595 160  
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly  
 1605 1610 1615  
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro  
 1620 1625 1630  
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln  
 1635 1640 1645  
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile  
 1650 1655 1660  
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser  
 1665 1670 1675 168  
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn  
 1685 1690 1695  
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr  
 1700 1705 1710  
 Met Lys His Gln Ser Gln Leu  
 1715

&lt;210&gt; 379

&lt;211&gt; 656

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 379

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1 5 10 15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 20 25 30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60

Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
 355 360 365  
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu  
 370 375 380  
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys  
 385 390 395 400  
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu  
 405 410 415  
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn  
 420 425 430  
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro  
 435 440 445  
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu  
 450 455 460  
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu  
 465 470 475 480  
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp  
 485 490 495  
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu

500 505 510  
 Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys  
 515 520 525  
 Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly  
 530 535 540  
 Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser  
 545 550 555 560  
 Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr  
 565 570 575  
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln  
 580 585 590  
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln  
 595 600 605  
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys  
 610 615 620  
 Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile  
 625 630 635 640  
 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu  
 645 650 655

&lt;210&gt; 380

&lt;211&gt; 671

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 380

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1 5 10 15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 20 25 30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn

225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
 355 360 365  
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu  
 370 375 380  
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys  
 385 390 395 400  
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu  
 405 410 415  
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn  
 420 425 430  
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro  
 435 440 445  
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu  
 450 455 460  
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu  
 465 470 475 480  
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp  
 485 490 495  
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu  
 500 505 510  
 Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp  
 515 520 525  
 Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys  
 530 535 540  
 His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala  
 545 550 555 560  
 Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg  
 565 570 575  
 Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His  
 580 585 590  
 Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn  
 595 600 605  
 Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile  
 610 615 620  
 Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys  
 625 630 635 640  
 Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala  
 645 650 655  
 Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu  
 660 665 670

<210> 381  
 <211> 251  
 <212> DNA  
 <213> Homo sapien

<400> 381  
 ggagaagcgt ctgctggggc aggaaggggt ttccctgccc tctcacctgt ccctcaccaa 60  
 ggtaacatgc ttcccctaag ggtatcccaa cccagggggc tcaccatgac ctctgagggg 120  
 ccaatatccc aggagaagca ttggggaggt gggggcaggt gaaggacca ggactcacac 180  
 atcctggggc tccaaggcag aggagaggggt cctcaagaag gtcaggagga aaatccgtaa 240  
 caagcagtca g 251

<210> 382  
 <211> 3279  
 <212> DNA  
 <213> Homo sapiens

<400> 382  
 cttcctgcag ccccatgct ggtgaggggc acgggcagga acagtggacc caacatggaa 60  
 atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120  
 cactggggagg ggacatcctg cagaaggtag gagtgcagaa acaccgctg caggggaggg 180  
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggagggg 240  
 gggcctggag ggcgtgagga ggagcgaggg ggctgcatgg ctggagttag ggatcagggg 300  
 cagggcgcca gatggcctca cacagggaag agagggcccc tcctgcaggg cctcacctgg 360  
 gccacaggag gacactgctt ttctctgag gagtgcaggag ctgtggtatgg tgctggacag 420  
 aagaaggaca gggcctggct caggtgtcca gaggctgtcg ctggcttccc ttggggatca 480  
 gactgcaggg agggagggcg gcagggttgt ggggggagtg acgatgagga tgacctgggg 540  
 gtggctccag gccttgcccc tgctggggcc ctcacccagc ctccctcaca gtctcctggc 600  
 cctcagtctc tcccctccac tccatcctcc atctggcctc agtgggtcat tctgatcact 660  
 gaactgacca taccagccc tgcccacggc cctccatggc tcccacatgc cctggagagg 720  
 ggacatctag tcagagagta gtctgaaga ggtggcctct gcgatgtgcc tgtgggggca 780  
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 gagccttggt cctctgttg gactccctgc ccatattctt gtgggagtgg gttctggaga 960  
 catttctgct tgttctgag agctgggaat tgctctcagt catctgcctg cgcggttctg 1020  
 agagatggag ttgcctaggc agttattggg gccaatctt ctactgtgt ctctcctcct 1080  
 ttacccttag ggtgattctg ggggtccact tgtctgtaat ggtgtgcttc aaggtatcac 1140  
 atcatggggc cctgagccat gtgccctgcc tgaaaagcct gctgtgtaca ccaaggtggg 1200  
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 cccctacctc tagtaaat t aagtccacct cacgttctgg catcacttgg cctttctgga 1320  
 tgctggacac ctgaagcttg gaactcacct ggccgaagct cgagcctcct gagtccact 1380  
 gacctgtgct ttctggtgtg gagtccaggg ctgctaggaa aaggaatggg cagacacagg 1440  
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 tgtttgtggg gtgcagagat gggaggggtg gggcccaccc tggaagagtg gacagtga 1620  
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 tagggggaga aactgaaagc tgatttaatta caggaggttt gttcaggctc cccaaaccac 1860  
 cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggg 1920  
 ttattatggg ttgttacatt gataggatac atactgaaat cagcaaacaa aacagatgta 1980  
 tagattagag tggggagaaa acagaggaaa acttgacgtt acgaagactg gcaacttggc 2040  
 tttactaagt ttccagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100  
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```

gcataaccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaaagtaa ttccaactga ggaagctcac ctgaccccta 2280
gtgtccagggt tttttactgg gggctctgtag gacgagtatg gagtacttga ataattgacc 2340
tgaagtcttc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacagggg ttcatcacia atccccatctt tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaagtgc 2520
atctcccagg agttattcaa gggtagagccc ttacttggg atgtacagge tttgagcagt 2580
gcagggctgc tgagtcaacc ttttattgta caggggatga gggaaaggga gaggatgagg 2640
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aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcttt cttttcacac cattggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca cccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggatttg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
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gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagctga 3120
cccagctgat agaggaagta gccagggtgg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctgggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtgtt 3279

```

&lt;210&gt; 383

&lt;211&gt; 155

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 383

```

Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
          5                      10                      15

```

```

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
          20                      25                      30

```

```

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
          35                      40                      45

```

```

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
          50                      55                      60

```

```

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
          65                      70                      75                      80

```

```

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
          85                      90                      95

```

```

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
          100                     105                     110

```

```

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
          115                     120                     125

```

```

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
          130                     135                     140

```

```

Ala Leu Glu Arg Gly His Leu Val Arg Glu
          145                     150

```

<210> 384  
 <211> 557  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
 ggatcctcta gagcggcgcg ctactactac taaattcgcg gccgcgtcga cgaagaagag 60  
 aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg ttccaacca 120  
 ggggaagggt cccttttgca ttgccaagt ccataaccat gagcactact ctaccatgg 180  
 tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240  
 acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300  
 ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360  
 tccccaagac acatcctaaa aggtgttgta atgggtgaaaa cgtcttcctt ctttattgcc 420  
 ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480  
 tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540  
 aaaaaaaaaa aaaaaaa 557

<210> 385  
 <211> 337  
 <212> DNA  
 <213> Homo sapiens

<400> 385  
 ttcccagggt atgtgcgagg gaagacacat ttactatcct tgatggggct gatcccttta 60  
 gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120  
 tctcaaagcc atctgctgtc ttcgagtacg gacacatcaa cactcctgca ttgttgatca 180  
 aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240  
 tatcagacag gtccagtttc cgcaccaaca cctgctgggt ccctgtcgtg gtctggatct 300  
 ctttgccac caattcccc tttccacat cccggca 337

<210> 386  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 386  
 gggcccgcta cgggccagg cccgcctcg cgagtcctcc tccccgggtg cctgcccga 60  
 gccgcctcgg ccagagggt gggcgcgagg ctgcctctac cggctggcgg ctgtaactca 120  
 gcgaccttgg cccgaaggct ctgcaagga cccaccgacc ccagccgcgg cggcggcggc 180  
 gcggactttg cccggtgtgt ggggcggagc ggactgcgtg tccgcggacg ggcagcgaag 240  
 atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

<210> 387  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

<400> 387  
 gggccgagtc gggcaccaag ggactctttg caggcttcc tccctcgatc atcaaggctg 60  
 cccctcctg tgccatcatg atcagacct atgagttcgg caaaagcttc ttccagaggc 120  
 tgaaccagga ccggtctctg ggcggtgaa aggggcaagg aggcaggac cccgtctctc 180  
 ccacggatgg ggagagggca ggaggagacc cagccaagt ccttttcttc agcactgagg 240  
 gagggggctt gtttcccttc cctcccggcg acaagctcca gggcagggtc gtccctctg 300

```

gcggcccagc acttcctcag acacaacttc ttctgtctgc tccagtcgtg gggatcatca 360
cttaccacc cccaagttc aagaccaa atctccagctg ccccttcgt gttccctgt 420
gtttgtgtg gctgggcatg tctccaggaa ccaagaagcc ctccagcctg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaaa aaaaaaa 537

```

<210> 388

<211> 520

<212> DNA

<213> Homo sapiens

<400> 388

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aggataat ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgagggttaa ccagtttgca tccccctaat gtggaaaaag taaggaggact actcagcact 120
gtttgaagat tgctctctt acagcttctg agaattgtgt tatttcaact gccaaagtga 180
ggacccccct cccaacatgc ccagccccc cctaagcat ggctccctgt caccaggcaa 240
ccaggaaact gctacttgtg gacctcacca gagaccagga ggggttggtt agctcacagg 300
acttccccca cccagaaga ttagcatccc atactagact cataactcaac tcaactaggc 360
tcatactcaa ttgatgggta ttagacaatt ccatttcttt ctgggtatta taaacagaaa 420
atcttctctt ttctcattac cagtaaaggc tcttggtatc tttctgttg aatgatttct 480
atgaacttgt cttattttta tgggtgggtt ttttcttgt 520

```

<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

```

cgttgcccc gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagttaaggc tggatttcag atctgcttgg ttccagccgc agtgtgccct ctgctcccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttctctg ccttcagcaa ggggcgttg ccacattctc 300
tgagggtcag tggaagaacc tagactcca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

```

<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

```

tgctctcca tcttggcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacgntt ctcatgggtg tggaacatct ctgcttgagg ttccaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

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<210> 391

<211> 325

<212> DNA

<213> Homo sapiens



<220>  
<221> misc\_feature  
<222> (1)...(325)  
<223> n = A,T,C or G

<400> 391  
tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60  
ctctcgccccc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120  
tagccagggc actgctgcca acagccagtc cnnataccat catgtnaccc ggtgngctct 180  
naanttn gat ntccanagcc ctaccatcn tagttctgct ctcccaccgg ntaccagccc 240  
cactgcccag gaatcctaca gccagtaccc tgtcccgacg tctctaccta ccagtacgat 300  
gagacctccg gctactacta tgacc 325

<210> 392  
<211> 277  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(277)  
<223> n = A,T,C or G

<400> 392  
atattgttta actccttctt ttatatcttt taacattttc atggngaaaag gttcacatct 60  
agtctcactt nggcnagnn ctctacttg agtctcttcc cgggcctggn ccagtnghaa 120  
antaccanga accgncatgn cttaanaacn ncctgggttn tgggttnntc aatgactgca 180  
tgacgtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggagg 240  
ctgaggatag agcgccgcgt cctgtgttgc tggggaa 277

<210> 393  
<211> 566  
<212> DNA  
<213> Homo sapiens

<400> 393  
actagtccag tgtgggtggaa ttcgcgcccg cgtcgacgga caggtcagct gtctggctca 60  
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga tttaaattcag cctaaacgtt 120  
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180  
gagaaggctc agtttgtcca tcagcattat catgatatca ggactgggta cttgggttaag 240  
gaggggtcta ggagatctgt ccctttttaga gacaccttac ttataatgaa gtatttgga 300  
gggtgggttt caaaagtaga aatgtcctgt attccgatga tcacctctga aacattttat 360  
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420  
ttctgcctca atgtttactg tgcctttgtt ttgtctagtt tgtgtgtgtg aaaaaaaaaa 480  
cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540  
ttttgcctat caaaaaaaaaa aaaaaa 566

<210> 394  
<211> 384  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

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gaacatacat gtccccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaattnng gaccggggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggcttttaa ggagtttttaa gctgagtgtc actgtagacc ccaaatacca 180
tccaagatt atcggggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt 384
```

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

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ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct tccagttacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataacctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggt 360
gcagcctggt gagaccatcc aatcccaa ataatgcac 399
```

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

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tggagtnttc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtgagg gataaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403
```

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397  
actagtncag tgggtggaa ttgcgggccg cgtcgacctt naanccatct ctatagcaaa 60  
tccatccccg ctcttggttg gtnacagaat gactgacaaa 100

<210> 398  
<211> 278  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(278)  
<223> n = A,T,C or G

<400> 398  
gcggccgcgt cgacagcagt tccgccagcg ctgcaccttg ggtggggatg tgctgcacgc 60  
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacctcac ctggggcgat 120  
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgaggtgg actcatcatg 180  
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240  
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

<210> 399  
<211> 298  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(298)  
<223> n = A,T,C or G

<400> 399  
acggaggtgg aggaagcgnc cctgggacgt anaggatggg tcctgncatt gaccncctcn 60  
ggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120  
ccgagatcga gcgcattggc ctggatcatg accgcatggg ctccgtggag cgcattggct 180  
ccggcattga gcgcattggc ccgctgggcc tcgaccacat ggctccanc attganccga 240  
tgggcccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcatggg 298

<210> 400  
<211> 548  
<212> DNA  
<213> Homo sapiens

<400> 400  
acatcaacta ctctctcatt ttaaggtatg gcagttccct tcatcccttt ttcctgcctt 60  
gtacatgtac atgtatgaaa ttctcttctc ttaccgaact ctctccacac atcacaaggt 120  
caaagaacca cacgcttaga agggtaagag ggcacctat gaaatgaaat ggtgatttct 180  
tgagtcctct ttttccacgt ttaaggggac atggcaggac ttagagttgc gagttaagac 240  
tgagaggggc tagagaatta ttcatatagc gctttgaggc caccatgtc acttatcccc 300  
tataccctct caccatcccc ttgtctactc tgatgccccc aagatgcaac tgggcagcta 360  
gttggcccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420  
ctttccagtg atctctacc atgggccccc ctctgggat caagccctc ccaggccctg 480  
tcccagccc ctctgcccc agcccacccg cttgccttgg tgctcagccc tcccattggg 540  
agcaggtt 548

<210> 401  
<211> 355  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(355)  
<223> n = A,T,C or G

<400> 401  
actgtttcca tgttatgttt ctacacattg ctacctcagt gctcctggaa acctagcttt 60  
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120  
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180  
tataaatgaa tgtctgaag caaagtgtcc atgggtggcg cgaagaagan aaagatgtgt 240  
tttgttttgg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300  
cccttttgca ttgccaagtg ccataacat gagcactact ctaccatggn tctgc 355

<210> 402  
<211> 407  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(407)  
<223> n = A,T,C or G

<400> 402  
atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60  
tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120  
aaatggaaaa cagaaaaaag cagggtgttg actcctactt tctgacaaaa cagactatgc 180  
gaataaagat aaaaaagaga aggacattac aaagggtggtc ctgacctttg ataaatctca 240  
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300  
ttgtggagct tctccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360  
gntgatattg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403  
<211> 303  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(303)  
<223> n = A,T,C or G

<400> 403  
cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaattc aggcacaaaa 60  
tcctaagcaa gagccatggc atgggtgaaa tgcaaaaagg gagtctggcc aatctacaaa 120  
tagagaacaa gacctactca gtcataaaca aaaaggcaga caccaacatg gatctcatgg 180  
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240  
tcttaacaac gaccgaaacc cattatttac ataaacctcc attcggtaac catggtgaaa 300  
gga 303

<210> 404  
<211> 225  
<212> DNA  
<213> Homo sapiens

<400> 404  
aagtgtact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60  
attgttaatg cactcattta cctttacatg gtgaaagtgc tctcttgatc ctacaaacag 120  
acattttcca ctctgtgttc catagtgtt aagtgtatca gatgtgttg gcatgtgaat 180  
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405  
<211> 334  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(334)  
<223> n = A,T,C or G

<400> 405  
gagctgttat actgtgagtt ctactaggaa atcatcaaatt ctgagggttg tctggaggac 60  
ttcaatacac ctcccccat agtgaatcag cttccagggg gtccagtccc tctccttact 120  
tcattcccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180  
ttccagtgct ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtgt 240  
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300  
cactctccac tctctcanng tggatccac ccct 334

<210> 406  
<211> 216  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(216)  
<223> n = A,T,C or G

<400> 406  
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60  
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120  
acnaaacaca aattttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180  
actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407  
<211> 413  
<212> DNA  
<213> Homo sapiens

<400> 407  
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60  
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120  
gtacaacatt gcacccagtg tcagattcta caccctggcca ctcaggaagc aagagttaat 180  
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240

ggaaaaattgt catttggtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300  
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt ttctctgtca 360  
tgggagttcc agaaaaagtt aaaacagaca atggggccagg ttctgtagta aag 413

<210> 408

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(183)

<223> n = A,T,C or G

<400> 408

ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60  
tntttaacta gttaatcctt aaagggctan ntaatcctta actagtcctt ccattgtgag 120  
cattatcctt ccagtattcn ccttctnttt tatttactcc ttcttggtta cccatgtact 180  
ntt 183

<210> 409

<211> 250

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 409

cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60  
gtggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120  
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180  
gcttcccagt gccccagga cagcgtgggc tatgtttaca ggccttcctt gctggggggg 240  
ggcctatgc 250

<210> 410

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(306)

<223> n = A,T,C or G

<400> 410

ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60  
agtcttgcaa tccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120  
cccagggacc ttggaaacag ttggcactgt aagggtgctt ctccccaaga cacatcctaa 180  
aagggtgtgt aatggtgaaa accgcttctt tctttattgc cccttcttat ttatgtgaac 240  
nactgggttg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300  
tcntgc 306

<210> 411  
<211> 261  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(261)  
<223> n = A,T,C or G

<400> 411  
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60  
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120  
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180  
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240  
cttctctcaa ggngaggcaa a 261

<210> 412  
<211> 241  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(241)  
<223> n = A,T,C or G

<400> 412  
gttcaatgtt acctgacatt tctacaacac cccactcacc gatgtattcg ttgcccagtg 60  
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt ctgcccagg aaatactacg 120  
actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180  
ctgggagatt tactgggta cattgaattc caaaactacc cangcaatta cccagccaac 240  
a 241

<210> 413  
<211> 231  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(231)  
<223> n = A,T,C or G

<400> 413  
aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60  
ctcatccaag ttcttagtac ctctctttg ttgtgaagga taatcaaact gaacaacaaa 120  
aagtttactc tctctattg gaacctaaaa actctcttct tctgggtct gagggctcca 180  
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414  
<211> 234  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 414

```
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca      234
```

&lt;210&gt; 415

&lt;211&gt; 217

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(217)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 415

```
gcataggatt aagactgagt atcttttcta cattctttta actttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggg tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc      217
```

&lt;210&gt; 416

&lt;211&gt; 213

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(213)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 416

```
atgcataatnt aaagganact gcctcgtttt tagaagacat ctggngctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctcccttc agactattac 120
cgaatgcaag gtgggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag      213
```

&lt;210&gt; 417

&lt;211&gt; 303

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(303)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 417

```
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaate tccaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggtc 240
tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
agt      303
```



<210> 418  
<211> 328  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(328)  
<223> n = A,T,C or G

<400> 418  
tttttggcgg tggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60  
tgcacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120  
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacacca gctagttttt 180  
gtatttttag tagagacagg gtttcacat gttggccagg ctggtctcaa actcctnacc 240  
tcagnggtca ggctggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300  
aaagtgctan gattacaggc cgtgagcc 328

<210> 419  
<211> 389  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(389)  
<223> n = A,T,C or G

<400> 419  
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatattg 60  
acccttgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120  
cttgtttctt ctctgtggct ccattcatag cacagtgtt gcactgaggc ttgtgcaggc 180  
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240  
ccggttctcc agccaccaac ctactcgtc cccgcaaata gcacatcagt tcttctaccg 300  
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360  
tggcagccac tcnggctgtg tcgacgcgg 389

<210> 420  
<211> 408  
<212> DNA  
<213> Homo sapiens

<400> 420  
gttcctccta actcctgcc aaaacagctc tcctcaacat gagagctgca cccctcctcc 60  
tggccagggc agcaagcctt agccttggct tctgtttct gctttttttc tggctagacc 120  
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180  
gtcccattga cacttttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240  
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300  
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360  
acgttgaccg gactttgatg aagtgtatg acaaacctgg caagccccg 408

<210> 421  
<211> 352  
<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 421

```
gctcaaaaat ctttttactg atnnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggtct tttttgggtc cttcttctcc accacnatat acttgagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacaggtg tagaaacaag 240
ggtgcaacat gaaatttctg ttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttctt gg 352
```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```
atgccaccat gctggcaatg cagcggggcg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcggcgg cgtcaatcct ggccaaggct agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggct 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gtttcttccg ccggtacggc tggcctatga aaattat 337
```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(310)

<223> n = A,T,C or G

<400> 423

```
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggcctggcct gggagccctg tgcctactan aagcncatta gattatccat 120
tcactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagtta 310
```

<210> 424

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(370)

<223> n = A,T,C or G

&lt;400&gt; 424

```

gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
ccttcttgaa gattctttgg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctgggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaagggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg                                     370

```

&lt;210&gt; 425

&lt;211&gt; 216

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(216)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 425

```

aattgctatn ntattatttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaata 60
taacaacnca acatcaaggn aaananaaca ggaatggntg acntgcata aatnggccga 120
anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtntntg aggagg                                     216

```

&lt;210&gt; 426

&lt;211&gt; 596

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 426

```

cttccagtgga ggataaccct gttgccccgg gccgagggtc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gcccgaaggg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatggtga 180
gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca cttcccgtta 300
ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcaactgc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattgggt tactgcctga 540
gtcccgcgtgg tcccattcca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

```

&lt;210&gt; 427

&lt;211&gt; 107

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(107)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 427

```

gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncctag 60

```

cccgaggagca gccttanaga gctcctgttt gactgcccgg ctcagng 107

<210> 428  
<211> 38  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(38)  
<223> n = A,T,C or G

<400> 428  
gaacttcna anaangactt tattcactat ttacatt 38

<210> 429  
<211> 544  
<212> DNA  
<213> Homo sapiens

<400> 429  
ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60  
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120  
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180  
tttggtggtt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240  
gccttccact tcagttacac ctactcacc atcctctcct gttggttctg tctgtcttca 300  
agataactaag ccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360  
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420  
gagtttagtt caaagcagta ttcagcgatt tcaagagaag tttttatatt ttgctttgac 480  
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccagggtg gtaggagaga 540  
ttat 544

<210> 430  
<211> 507  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(507)  
<223> n = A,T,C or G

<400> 430  
cttatcncaa tggggctccc aaacttggtt gtgcagtgga aactccgggg gaattttgaa 60  
gaacactgac acccatcttc caccocgaca ctctgattta attgggctgc agtgagaaca 120  
gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttctg atctttgccc 180  
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgagggg gttccaggag 240  
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300  
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360  
tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420  
cattctcttc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480  
ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431  
<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 431

```
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcacc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgtgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggcttttac tctgctgttt ct 392
```

<210> 432

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(387)

<223> n = A,T,C or G

<400> 432

```
ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcggn a gtccagccac tngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgctctnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccttt 387
```

<210> 433

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(281)

<223> n = A,T,C or G

<400> 433

```
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagngagg ntctctgtnt gccactggg 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281
```

<210> 434

<211> 484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 434

```
ttttaaaata agcatttagt gctcagtcct tactgagtag tctttctctc ccttctcttg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca ttctactgtg atgtatattg 120
tggtgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtaga tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaacccat ttcacccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
ttta
```

484

&lt;210&gt; 435

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 435

```
gcgcccgtca gagcaggta ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaaccct cctcctcgcc gacttcggaa ctggcgagag ttcagcgag 180
atgggctgtt ggggaggggg caagatagat gaggggggag ggcattggtc ggggtgacc 240
cttgagagga ggaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggcct 300
ggtagagacc tttgggggtc tggaaacctt ggactcccca tgctctaact cccacactct 360
gctatcagaa acttaaacct gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac
```

424

&lt;210&gt; 436

&lt;211&gt; 667

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(667)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 436

```
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataaggggtg 120
agcctcttct ggaattcttc tgatttcaaa gtctcactct caagtctctg aaaacggagg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggtc 300
gccaggtttg tcatagcact catcaaagtc cggtaacgt ctgtgcttcg aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatctc tctttcttat atactctcca 420
agttcataat gctgtcccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaagggt tcaatgggac ttcggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctcttggtt agtacacttc ggtctagcca gaaaaaagg 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tggtgag
```

667

&lt;210&gt; 437

&lt;211&gt; 693

<212> DNA

<213> Homo sapiens

<400> 437

```
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc acactaggac tctaccatac cggggtttgt 120
taaagctcag gtaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtaactct ctattttcac cctcttgct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcatc tttagctttc 420
atgtgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
tctattttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc                                     693
```

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

```
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac cttcgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgccca aagaatcttc aagaaggagg 180
actgcaagta tatctgggtg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagc ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360
```

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

```
gttcctnnta actcctgccca gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttgget tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgt gtttcggcat ggagaccgaa 180
gtcccatgta cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aathtagtag t                                     431
```

<210> 440

<211> 523

<212> DNA

<213> Homo sapiens

&lt;400&gt; 440

```
agagataaag cttagggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaaac 360
taaaaaattaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcactctg tgagaacaag cta 523
```

&lt;210&gt; 441

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 441

```
gttcctccta actcctgcc a gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtc tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccatatga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attccttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatcttagtag 430
```

&lt;210&gt; 442

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 442

```
ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcttgga tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362
```

&lt;210&gt; 443

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(624)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 443

```
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
```



```

cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaataaac 360
taacgcctac aaaacactta aacatagata acatagggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatac                                     624

```

```

<210> 444
<211> 425
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(425)
<223> n = A,T,C or G

```

```

<400> 444
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgtgt gtcagcaaata ccttgaatgc 180
tgcttaattgt gagagggttg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgtgtg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcatcctgt gaagagccaa 360
ggaggcacca gggcataagt gactagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga                                     425

```

```

<210> 445
<211> 414
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(414)
<223> n = A,T,C or G

```

```

<400> 445
catgtttatg nttttggatt actttgggca cctagtgttt ctaaactgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcattgtggc agattatttg atgtagtctt cttaaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggcttctcc tcttgtattt tgaagcagtg 360
tggtgtgttg attgataaaa aaaaaaaaaa tcgacgcggc cgcaatttta gtag      414

```

```

<210> 446
<211> 631
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(631)

```

<223> n = A,T,C or G

<400> 446

```
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcagggtgtg 120
atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtgggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaaccttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttggga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccttg catttgtggg 540
aatctacacc aatgaaaaca tgtactacag ctatatgtga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g 631
```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1) ... (585)

<223> n = A,T,C or G

<400> 447

```
ccttgggaaa antntcacia tataaagggt cgtagacttt actccaaatt ccaaaaagggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagtcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240
tgggctgcca gaggtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccaggtttgt catagactc atcaaagtcc ggtcaacgtc tgtgcttga atataaacct 360
gttcagtgtt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggtca gtacacttcg gtcta 585
```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1) ... (93)

<223> n = A,T,C or G

<400> 448

```
tgctcgtggg tcattctgan nccgaactg accntgccag ccctgccgan gggccnccat 60
ggctccctag tgcctggag agganggggc tag 93
```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(706)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 449

```
ccaagttcat gctntgtgct ggacgctgga cagggggcaa aagcnnttgc tcgtgggtca 60
ttctgancac cgaactgacc atgccagccc tgccgatggc cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtcctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggtcgggcg cgtccattc gccattcagg ctgcgcaact 240
gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcncga cggtgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcatgcacg 420
cgtacgtaag ctrggatect ctagagcggc cgccactac tactaaattc gcggccgctg 480
cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncccca 660
gcattgatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa 706
```

&lt;210&gt; 450

&lt;211&gt; 493

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 450

```
gagacggagt gtcactctgt tggccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
acagttttta aaggtaaaac aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
aaatgaggct gagaacttta caaagggatc ttacagacat gtccccaata tcaactgcatg 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
caagtcaggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagtgag ttctatccat gaggtgattc cacagtcttc 360
tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480
gcgaatttag tag 493
```

&lt;210&gt; 451

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 451

```
gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cggcgcgggc 60
ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
aacgccaggg ttttccagc cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
cgcncagac actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420
gttgcaatga gctgagatca ggcnctgcn cccagcatg gatgacagag tgaaactcca 480
```

tcttaaaaaa aaaaaaaaaa a

501

<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(51)

<223> n = A,T,C or G

<400> 452

agacggtttc accnttacaa cnccttttag gatgggnntt ggggagcaag c

51

<210> 453

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(317)

<223> n = A,T,C or G

<400> 453

tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60  
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaaccat 120  
ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180  
taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240  
cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300  
taccatgtc tttatta 317

<210> 454

<211> 231

<212> DNA

<213> Homo sapiens

<400> 454

ttcgaggtag aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60  
taagccacgc cagctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120  
agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180  
ccttcctttt tcagtgttcc aaagctctc acaatttcat gaacaacagc t 231

<210> 455

<211> 231

<212> DNA

<213> Homo sapiens

<400> 455

taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60  
cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120  
gtttcaacgc attgatgact tctccaagga ttttcttttg gcatcgacca cattcagggg 180  
caaagaattt ctcatagcac agctcacaat acagggtctc ttttctctct a 231

<210> 456  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 456  
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60  
ttccattcag tattatcggt attattcttg gagaaaccct gtctgtttac tgtaaccttt 120  
tgcactcaaa ttcctttatc aggaataact acatagccac tatttacaaa gccattggaa 180  
cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaag t 231

<210> 457  
<211> 231  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(231)  
<223> n = A,T,C or G

<400> 457  
cgaggtagcc aggggtctga aaatctctnn tttantagtc gatagcaaaa ttgttcacatca 60  
gcattcctta atatgatctt gctataatta gattttcttc cattagagtt catacagttt 120  
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180  
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgc g 231

<210> 458  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 458  
aggctctggt cccccactt ccactccctt ctactctctc taggactggg ctgggccaaag 60  
agaagagggg tgggttaggga agccgttgag acctgaagcc ccacctcta ccttccttca 120  
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180  
ggtcctgggt taggcatttt ggggggccag accccaggag aagaagattc t 231

<210> 459  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 459  
ggtaccgagg ctctctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60  
ccttcgcgaa acctgtggtg gccaccagt cctaacggga caggacagag agacagagca 120  
gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180  
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 460

gcaggtataa catgctgcaa caacagatgt gactaggaac ggccgggtgac atggggaggg 60  
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaa 120  
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180  
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231

<210> 461

<211> 231

<212> DNA

<213> Homo sapiens

<400> 461

cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggaggggtc 60  
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcttg tgtgtcctgg 120  
gtgggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag 180  
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231

<210> 462

<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60  
gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120  
gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag tcttacattt 180  
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

<400> 463

tactccagcc tggtgacaga gcgagaccct atcaccgccc cccaccccac caaaaaaaaa 60  
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<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

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<211> 231

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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&lt;210&gt; 469

&lt;211&gt; 2229

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 469

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&lt;210&gt; 470

&lt;211&gt; 2426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 470

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2426

&lt;210&gt; 471

&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 471

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812

&lt;210&gt; 472

&lt;211&gt; 515

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (1)...(515)

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&lt;400&gt; 472

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